

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtels, Kim
- (ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
- (iii) NUMBER OF SEQUENCES: 231
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sprunger, Suzanne A.
 - (B) REGISTRATION NUMBER: 41,323
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2043 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGAATGCCC	CATGCGCACC	CCACAGCTCG	CGCTCCTGCA	AGTGTCTTTT	CTGGTGTTC	60
CCGATGGCGT	CCGGCCTCAG	CCCTCTTCCT	CCCCATCAGG	GGCAGTGCCC	ACGTCTTTGG	120
AGCTGCAGCG	AGGGACGGAT	GGCGGAACCC	TCCAGTCCCC	TTCAGAGGCG	ACTGCAACTC	180
GCCCCGCCGT	GCCTGGACTC	CCTACAGTGG	TCCCTACTCT	CGTGACTCCC	TCGGCCCCCTG	240
GGAATAGGAC	TGTGGACCTC	TTCCCAGTCT	TACCGATCTG	TGTCTGTGAC	TTGACTCCTG	300
GAGCCTGCGA	TATAAATTGC	TGCTGCGACA	GGGACTGCTA	TCTTCTCCAT	CCGAGGACAG	360
TTTTCTCCTT	CTGCCTTCCA	GGCAGCGTAA	GGTCTTCAAG	CTGGGTTTGT	GTAGACAACT	420
CTGTTATCTT	CAGGAGTAAT	TCCCCGTTTC	CTTCAAGAGT	TTTCATGGAT	TCTAATGGAA	480
TCAGGCAGTT	TTGTGTCCAT	GTGAACAACT	CAAACCTAAA	CTATTTCCAG	AAGCTTCAAA	540
AGGTCAATGC	AACCAACTTC	CAGGCCCTGG	TTGCAGAGTT	TGGAGGCGAA	TCATTCACTT	600
CAACATTCCA	AACTCAATCA	CCACCATCTT	TTTACAGGGC	CGGGGACCCC	ATTCTTACTT	660
ACTTCCCCAA	GTGGTCTGTA	ATAAGCTTGC	TGAGACAACC	TGCAGGAGTT	GGAGCTGGGG	720
GACTCTGTGC	TGAAAGCAAT	CCTGCAGGTT	TCCTAGAGAG	TAAAAGTACA	ACTTGCACTC	780
GTTTTTTTCA	AGAACCTGGC	TAGTAGCTGT	ACCTTGGATT	CAGCCCTCAA	TGCTGCCTCT	840
TACTATAACT	TCACAGTCTT	AAAGGTTCCA	AGAAGCATGA	CTGATCCACA	GAATATGGAG	900
TTCCAGGTTT	CTGTAATACT	TACCTCACAG	GCTAATGCTC	CTCTGTGGC	TGGAAACACT	960
TGTCAGAAATG	TAGTTTCTCA	GGTCACCTAT	GAGATAGAGA	CCAATGGGAC	TTTTGGAATC	1020
CAGAAAGTTT	CTGTCAGTTT	GGGACAAACC	AACCTGACTG	TTGAGCCAGG	CGCTTCCTTA	1080
CAGCAACACT	TCATCCTTCG	CTTCAGGGCT	TTTCAACAGA	GCACAGCTGC	TTCTCTCACC	1140
AGTCCTAGAA	GTGGGAATCC	TGGCTATATA	GTTGGGAAGC	CACTCTTGGC	TCTGACTGAT	1200
GATATAAGTT	ACTCAATGAC	CCTCTTACAG	AGCCAGGGTA	ATGGAAGTTG	CTCTGTAAAA	1260
AGACATGAAG	TGCAGTTTGG	AGTGAATGCA	ATATCTGGAT	GCAAGCTCAG	GTTGAAGAAG	1320
GCAGACTGCA	GCCACTTGCA	GCAGGAGATT	TATCAGACTC	TTCATGGAAG	GCCCAGACCA	1380
GAGTATGTTG	CCATCTTTGG	TAATGCTGAC	CCAGCCCAGA	AAGGAGGGTG	GACCAGGATC	1440
CTCAACAGGC	ACTGCAGCAT	TTCAGCTATA	AACTGTACTT	CCTGCTGTCT	CATACCAGTT	1500
TCCCTGGAGA	TCCAGGTATT	GTGGGCATAT	GTAGGTCTCC	TGTCCAACCC	GCAAGCTCAT	1560

GTATCAGGAG TTCGATTCTT ATACCAGTGC CAGTCTATAC AGGATTCTCA GCAAGTTACA 1620
 GAAGTATCTT TGACAACTCT TGTGAACTTT GTGGACATTA CCCAGAAGCC ACAGCCTCCA 1680
 AGGGGCCAAC CCAAAATGGA CTGGAAATGG CCATTGACT TCTTCCCTT CAAAGTGGCA 1740
 TTCAGCAGAG GAGTATTCTC TCAAAAATGC TCAGTCTCTC CCATCCTTAT CCTGTGCCTC 1800
 TTAGAACTTG GAGTTCTCAA CCTAGAGACT ATGTGAAGAA AAGAAAATAA TCAGATTTCA 1860
 GTTTTCCCTA TGAGAACTC TGAGGCAGCC ACTTATCTTG GCTAAATAGA ACCTCACCTG 1920
 CTCATGACCA GAGAGCATTT AGGATAATAG AGGACCTAAC TGAAGGAATC CTTGTATATG 1980
 AAAGGAGTTA TTTTAGAAAA GCAATAAAAA TATTTTATTC ATCATAAAAA AAAAAAAAAA 2040
 AAA 2043

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Thr	Pro	Gln	Leu	Ala	Leu	Leu	Gln	Val	Phe	Phe	Leu	Val	Phe
1				5					10					15	
Pro	Asp	Gly	Val	Arg	Pro	Gln	Pro	Ser	Ser	Ser	Pro	Ser	Gly	Ala	Val
			20					25					30		
Pro	Thr	Ser	Leu	Glu	Leu	Gln	Arg	Gly	Thr	Asp	Gly	Gly	Thr	Leu	Gln
			35				40					45			
Ser	Pro	Ser	Glu	Ala	Thr	Ala	Thr	Arg	Pro	Ala	Val	Pro	Gly	Leu	Pro
			50				55				60				
Thr	Val	Val	Pro	Thr	Leu	Val	Thr	Pro	Ser	Ala	Pro	Gly	Asn	Arg	Thr
65					70					75					80
Val	Asp	Leu	Phe	Pro	Val	Leu	Pro	Ile	Cys	Val	Cys	Asp	Leu	Thr	Pro
				85					90					95	
Gly	Ala	Cys	Asp	Ile	Asn	Cys	Cys	Cys	Asp	Arg	Asp	Cys	Tyr	Leu	Leu
			100					105					110		
His	Pro	Arg	Thr	Val	Phe	Ser	Phe	Cys	Leu	Pro	Gly	Ser	Val	Arg	Ser
			115					120				125			
Ser	Ser	Trp	Val	Cys	Val	Asp	Asn	Ser	Val	Ile	Phe	Arg	Ser	Asn	Ser

130	135	140
Pro Phe Pro Ser Arg Val Phe Met Asp Ser Asn Gly Ile Arg Gln Phe		
145	150	155 160
Cys Val His Val Asn Asn Ser Asn Leu Asn Tyr Phe Gln Lys Leu Gln		
	165	170 175
Lys Val Asn Ala Thr Asn Phe Gln Ala Leu Val Ala Glu Phe Gly Gly		
	180	185 190
Glu Ser Phe Thr Ser Thr Phe Gln Thr Gln Ser Pro Pro Ser Phe Tyr		
	195	200 205
Arg Ala Gly Asp Pro Ile Leu Thr Tyr Phe Pro Lys Trp Ser Val Ile		
	210	215 220
Ser Leu Leu Arg Gln Pro Ala Gly Val Gly Ala Gly Gly Leu Cys Ala		
	225	230 235 240
Glu Ser Asn Pro Ala Gly Phe Leu Glu Ser Lys Ser Thr Thr Cys Thr		
	245	250 255
Arg Phe Phe Gln Glu Pro Gly		
	260	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGCAGCTCA TCAACCCCTT TGGAGAGGAT GATGATGATT TTGAGACCAA CTGGATTGTC	60
GACAGGAATT TGCAGGTGTC CCTGTTGGCT GTGGATGAGA TGCACCAGGA CCTGCCTCGG	120
ATGGAGCCGG ACATGTACTG GAATAAGCCC GAGCCACAGC CCCCCTACAC AGCTGCTTCC	180
GCCCAGTTCC GTCGAGCCTC CTTTATGGGC TCCACCTTCA ACATCAGCCT GAACAAAGAG	240
GAGATGGAGT TCCAGCCCAA TCAGGAGGAC GAGGAGGATG CTCACGCTGG CATCATTGGC	300
CGCTTCCTAG GCCTGCAGTC CCATGATCAC CATCCTCCCA GGGCAAATC AAGGACCAAA	360
CTACTGTGGC CCAAGAGGGA ATCCCTTCTC CACGAGGGCC TGCCCCAAAA CCACAAGGCA	420
GCCAAACAGA ACGTTAGGGG CCAGGAAGAC AACAAGGCCT GGAAGCTTAA GGCTGTGGAC	480
GCCTTCAAGT CTGCCCCACT GTATCAGAGG CCAGGCTACT ACAGTGCCCC ACAGACGCCC	540

CTCAGCCCCA CTCCCATGTT CTTCCCCCTA GAACCATCAG CGCCGTCAAA GCTTCACAGT 600
 GTCACAGGCA TAGACACCAA AGACAAAAGC TTAAAGACTG TGAGTTCTGG GGCCAAGAAA 660
 AGTTTTGAAT TGCTCTCAGA GAGCGATGGG GCCTTGATGG AGCACCCAGA AGTATCTCAA 720
 GTGAGGAGGA AACTGTGGA GTTTAACCTG ACGGATATGC CAGAGATCCC CGAAAATCAC 780
 CTCAAAGAAC CTTTGAACA ATCACCAACC AACATACACA CTACACTCAA AGATCACATG 840
 GATCCTTATT GGGCCTTGGA AAACAGGGAT GAAGCACATT CCTAACCTGC TTCCTAATGG 900
 GGATGCTTCG CCAGCCAGGT CCTCACCTGT GTGTACACCA GCAGGACACT GATCCAGTCA 960
 CAGCCATACA GCTGTCCACA CTGAAGAACA TGTCTTACAA CAGCCTGAAT CAAATGGCTA 1020
 GCTTAATAGA TAAAAATCCC AGACTACTTC AGCCTTTAAT GCCTTTTATT CATAAAAACT 1080
 GTGAAAGCTA GACTGAACCA TTGGAAACAT TTAATCAGA CTCTGGATTC AGAGTCGGGA 1140
 ACCCTTAGTT CTATCTGAAT CCAAGACAGC CACACCTTAG TATACTGCCC AAATAATGA 1200
 GTTTAATAAA TACAAATACT CGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1260
 AAA 1263

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	His	Gln	Asp	Leu	Pro	Arg	Met	Glu	Pro	Asp	Met	Tyr	Trp	Asn	Lys
1				5				10						15	
Pro	Glu	Pro	Gln	Pro	Pro	Tyr	Thr	Ala	Ala	Ser	Ala	Gln	Phe	Arg	Arg
			20					25					30		
Ala	Ser	Phe	Met	Gly	Ser	Thr	Phe	Asn	Ile	Ser	Leu	Asn	Lys	Glu	Glu
		35					40					45			
Met	Glu	Phe	Gln	Pro	Asn	Gln	Glu	Asp	Glu	Glu	Asp	Ala	His	Ala	Gly
	50					55					60				
Ile	Ile	Gly	Arg	Phe	Leu	Gly	Leu	Gln	Ser	His	Asp	His	His	Pro	Pro
65					70					75				80	

Arg Ala Asn Ser Arg Thr Lys Leu Leu Trp Pro Lys Arg Glu Ser Leu
 85 90 95
 Leu His Glu Gly Leu Pro Lys Asn His Lys Ala Ala Lys Gln Asn Val
 100 105 110
 Arg Gly Gln Glu Asp Asn Lys Ala Trp Lys Leu Lys Ala Val Asp Ala
 115 120 125
 Phe Lys Ser Ala Pro Leu Tyr Gln Arg Pro Gly Tyr Tyr Ser Ala Pro
 130 135 140
 Gln Thr Pro Leu Ser Pro Thr Pro Met Phe Phe Pro Leu Glu Pro Ser
 145 150 155 160
 Ala Pro Ser Lys Leu His Ser Val Thr Gly Ile Asp Thr Lys Asp Lys
 165 170 175
 Ser Leu Lys Thr Val Ser Ser Gly Ala Lys Lys Ser Phe Glu Leu Leu
 180 185 190
 Ser Glu Ser Asp Gly Ala Leu Met Glu His Pro Glu Val Ser Gln Val
 195 200 205
 Arg Arg Lys Thr Val Glu Phe Asn Leu Thr Asp Met Pro Glu Ile Pro
 210 215 220
 Glu Asn His Leu Lys Glu Pro Leu Glu Gln Ser Pro Thr Asn Ile His
 225 230 235 240
 Thr Thr Leu Lys Asp His Met Asp Pro Tyr Trp Ala Leu Glu Asn Arg
 245 250 255
 Asp Glu Ala His Ser
 260

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTTGAGGGT TTTTGTGTTTT TTGTTTTTTC TAGGATTCA TTGTGATGTT TTGGTTTTGT 60
 TTTTGTGCTTT TTGTTTAAGT TGTGCTGACA CCAAACACAT CCAGTTTATA ATCAGTACAT 120
 TGGAAAGCTG GTATTGATGT AGAACCAGTG CATAACTTTT TATGGGGTTT TGTTATTGGT 180

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TTTTTTTTTG TAAAGTGTGA ATAAAAGGTA TGTTTACTCA TTTTTCCTGA ACACTGTGTT      240
GGTAATGTGC ATCATGACAA TTTCCAGTGA AGGTGAGCTG GAGCTGGTTG GACTAATGAG      300
ACTGAGGAAG CAGCTTTTCC TACGATCTGC ATTATGTAAT CACAGGTCCA GAGAGCTTTA      360
TGGAAGCGGG AGAGGAGGAG CACTTACTCA TGTTGTATTT GTTAATGGAG GATGTCATCT      420
TTTCATAGAT GCTGGAAC TAAGTGCACCT GTTAGATGCT AAAGGTTTGA GCTTTACACA      480
AAATGTCTTC ATCTGTATTT GTTATTGTCT ACAATATATT TGAATTTGGG GCAGCATATT      540
AAGATGTAAT GCCCTGTTAT GTCTGGAAAA AACTTGTTTTT GCTTCTTCCA GGCAAAGGGC      600
ATTTTGTGGA TCAGTTTGAA CAGCTTCTCC ACCTTATTTG GACAGTGATA AATTGAACCA      660
AGAGTGTAGA TTTACAAGTG TAACCTTCAA AAGAGGAAGA ACTATTTGGG GTCTGTAGGT      720
AATGAACAGT CACACCAAAA TAGACTATGA TGCTTTTGTT AAGAAAGGTT TCATGTTTTA      780
GATATTTTCC GTGTCCTAAA TAATTTTCAA TAATCTATAA TCCCTAAAAT GCAATAAAAA      840
CTAGTATGTT TTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA      894

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Cys Ile Met Thr Ile Ser Ser Glu Gly Glu Leu Glu Leu Val Gly
1             5             10             15
Leu Met Arg Leu Arg Lys Gln Leu Phe Leu Arg Ser Ala Leu Cys Asn
20            25            30
His Arg Ser Arg Glu Leu Tyr Gly Ser Gly Arg Gly Gly Ala Leu Thr
35            40            45
His Val Val Phe Val Asn Gly Gly Cys His Leu Phe Ile Asp Ala Gly
50            55            60
Thr Arg Val His Leu Leu Asp Ala Lys Gly Leu Ser Phe Thr Gln Asn
65            70            75            80
Val Phe Ile Cys Ile Cys Tyr Cys Leu Gln Tyr Ile
85            90

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCCGCAG GTCTACTTGT GGCGAGCAGT CCAGCACAGC CTCACAGTGC AGAGCATGAG 60
CTTTGGAGCC TGCCCCCACC CTAGCTTTGT GACCTTAAGT GAGCTACATA GCTTCTCATG 120
TGTAAGTAC TCATCATAAT GGTTC TGACC TCAGTGGTTT GTTGTGTTCT AGGAAATGAT 180
GCCAGTGAAT GCGTAGTCCC AGCCTCAGCA CAGGGGAGCC ACCTTGAAGC TCTCAAATAT 240
CACTGTTGTG AATACAGAGA GGGAAAACCA ACTGTAACGT GCCACCCAAA TTTTTCAGA 300
TTAATACATC ATTCATCAGA CTTCAATTCGT GATCTCGAAG AGTGACATCA GTCTTCCTTG 360
GAATATGAAG AGAATTTCTT TGGTTCCTTCT TTTGCATTTT TATTTGATTT ATTTTATTTT 420
ATTTTATTTT ATGTTTTTTTGT GTACAGAAAAG CTCATTACTA GTCCTGTCCA GCAACGTGCC 480
TCTCCTGGCC CTAGAGTTCT TGGAAATAGC CCAGGCCAAA GAGAAGGCCT TTCTCCCCAT 540
GGTCAGCCAC ACGTTCCACA TGCGCACAGA GGAGTCTGAT GCCTCACAGG AGGGCGATGA 600
CCTACCCAAG TCCTCAGCAA ACACCAGCCA TCCCAAGCAG GATGACAGCC CCAAGTCCTC 660
AGAAGAAACC ATCCAGCCCA AGGAGGGTGA CATCCCCAAG GCCCCAGAAG AAACCATCCA 720
ATCCAAGAAG GAGGACCTCC CCAAGTCCTC GGAAAAAGCC ATCCAGCCCA AAGAGAGTAA 780
CATC 784

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Arg Ile Ser Leu Val Leu Leu Leu His Phe Tyr Leu Ile Tyr
1 5 10 15

Phe	Ile	Leu	Phe	Tyr	Phe	Met	Phe	Phe	Gly	Thr	Glu	Ser	Ser	Leu	Leu	
		20						25					30			
Val	Leu	Ser	Ser	Asn	Val	Pro	Leu	Leu	Ala	Leu	Glu	Phe	Leu	Glu	Ile	
		35					40					45				
Ala	Gln	Ala	Lys	Glu	Lys	Ala	Phe	Leu	Pro	Met	Val	Ser	His	Thr	Phe	
		50				55					60					
His	Met	Arg	Thr	Glu	Glu	Ser	Asp	Ala	Ser	Gln	Glu	Gly	Asp	Asp	Leu	
	65				70					75					80	
Pro	Lys	Ser	Ser	Ala	Asn	Thr	Ser	His	Pro	Lys	Gln	Asp	Asp	Ser	Pro	
				85					90					95		
Lys	Ser	Ser	Glu	Glu	Thr	Ile	Gln	Pro	Lys	Glu	Gly	Asp	Ile	Pro	Lys	
			100					105					110			
Ala	Pro	Glu	Glu	Thr	Ile	Gln	Ser	Lys	Lys	Glu	Asp	Leu	Pro	Lys	Ser	
			115				120					125				
Ser	Glu	Lys	Ala	Ile	Gln	Pro	Lys	Glu	Ser	Asn	Ile					
		130			135						140					

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAA	75

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGAAGAAGTA GAAGCATCGA AAGCGTTGGA GAGGTGTTAC CGGAACGGCG GCGACAAGGG	60
TGTTCCCGAA CTAGAGTGGG GCATACATAA TCTTGCTGCT ATGCTTCGAA GCTGTAGTCT	120
GAATCAACCT AAGTTTTTAA CAGAAGGTGA ACCTCTGAGA TAGAAAATCA AGTATATTTT	180

AAAAGAAGGG ATGTGGGATC AAGGAGGACA GCCTTGGCAG CAGTGGCCCT TGAACCAGCA 240
 ACAATGGATG CAGTCATTCC AGCACCAACA GGATCCAAGC CAGATTGATT GGGCTGCATT 300
 GGCCCAAGCT TGGATTGCCC AAAGAGAAGC TTCAGGACAG CAAAGCATGG TAGAACAACC 360
 ACCAGGAATG ATGCCAAATG GACAAGATAT GTCTACAATG GAATCTGGTC CAAACAATCA 420
 TGGGAATTTT CAAGGGGATT CAAACTTCAA CAGAATGTGG CAACCAGAAT GGGGAATGCA 480
 TCAGCAACCC CCACACCCCC CTCCAGATCA GCCATGGATG CCACCAACAC CAGGCCCCAAT 540
 GGACATTGTT CTCCTTCTG AAGACAGCAA CAGTCAGGAC AGTGGGGAAT TTGCCCTGA 600
 CAACAGGCAT ATATTTAACC AGAACAATCA CAACTTTGGT GGACCACCCG ATAATTTTGC 660
 AGTGGGGCCA GTGAACCAGT TTGACTATCA GGACCTCCAG GACCTCCAGC ACCTCCCCAG 720
 AATCGAAGAG AAAGGCCATC ATCATTCAGG GATCGTCAGC GTTCACCTAT TGCACTTCCT 780
 GTGAAGCAGG AGCCTCCACA AATTGACGCA GTAAACGCA GGACTCTTCC CGCTTGGATT 840
 CGCGAAGGTC TTGAAAAAAT GGAACGTGAA AAGCAGAAGA AATTGGAGAA AGAAAGAATG 900
 GAACAACAAC GTTCACAATT GTCCAAAAAA AAAAAAAAAA 939

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Trp Asp Gln Gly Gly Gln Pro Trp Gln Gln Trp Pro Leu Asn Gln
 1 5 10 15
 Gln Gln Trp Met Gln Ser Phe Gln His Gln Gln Asp Pro Ser Gln Ile
 20 25 30
 Asp Trp Ala Ala Leu Ala Gln Ala Trp Ile Ala Gln Arg Glu Ala Ser
 35 40 45
 Gly Gln Gln Ser Met Val Glu Gln Pro Pro Gly Met Met Pro Asn Gly
 50 55 60
 Gln Asp Met Ser Thr Met Glu Ser Gly Pro Asn Asn His Gly Asn Phe
 65 70 75 80
 Gln Gly Asp Ser Asn Phe Asn Arg Met Trp Gln Pro Glu Trp Gly Met

	85	90	95
His Gln Gln Pro Pro His Pro Pro Pro Asp Gln Pro Trp Met Pro Pro	100	105	110
Thr Pro Gly Pro Met Asp Ile Val Pro Pro Ser Glu Asp Ser Asn Ser	115	120	125
Gln Asp Ser Gly Glu Phe Ala Pro Asp Asn Arg His Ile Phe Asn Gln	130	135	140
Asn Asn His Asn Phe Gly Gly Pro Pro Asp Asn Phe Ala Val Gly Pro	145	150	155
Val Asn Gln Phe Asp Tyr Gln Asp Leu Gln Asp Leu Gln His Leu Pro	165	170	175
Arg Ile Glu Glu Lys Gly His His His Ser Gly Ile Val Ser Val His	180	185	190
Leu Leu His Phe Leu	195		

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGGAGAGCAG CCGGCAGCGC CTGGAGGCC CTGAGAGAGCT GCAATAAAGG AAGAAACAGA	60
ATATATGGAA CTTCTGGCAG CAGAAAAACA TCAAGTTGAA GCCCTTAAAA ATATGCAACA	120
TCAAAACCAA AGTTTATCCA TGCTTGACGA GATTCTTGAA GATGTAAGAA AGGCAGCGGA	180
TCGTCTGGAG GAAGAGATAG AGGAACATGC TTTTGACGAC AATAAATCAG TCAAGGGGGT	240
CAATTTTGAG GCAGTTCTGA GGGTGGAGGA AGAAGAGGCC AATTCTAAGC AAAATATAAC	300
AAAACGAGAA GTGGAGGATG ACTTGGGTCT TAGCATGCTG ATTGACTCCC AGAACAACCA	360
GTATATTTTG ACCAAGCCCA GAGATTCAAC CATCCCACGT GCAGATCACC ACTTTATAAA	420
GGACATTGTT ACCATAGGAA TGCTGTCCTT GCCTTGTGGC TGGCTATGTA CAGCCATAGG	480
ATTGCCTACA ATGTTTGGTT ATATTATTTG TGGTGTACTT CTGGGACCTT CAGGACTAAA	540
TAGTATTAAG TCTATTGTGC AAGTGGAGAC ATTAGGAGAA TTTGGGGTGT TTTTACTCT	600

TTTTCTTGTT	GGCTTAGAAT	TTTCTCCAGA	AAAGCTAAGA	AAGGTGTGGA	AGATTTCTCT	660
ACAAGGGCCG	TGTTACATGA	CACTGTTAAT	GATTGCATTT	GGCTTGCTGT	GGGGGCATCT	720
CTTGCGGATC	AAACCCACGC	AGAGCGTCTT	CATTTCCACG	TGTCTGTCCT	TGTCAAGCAC	780
ACCCCTCGTG	TCCAGGTTCC	TCATGGGCAG	TGCTCGGGGT	GACAAAGAAG	GCGACATTGA	840
CTACAGCACC	GTGCTCCTCG	GCATGCTGGT	GACGCAGGAC	GTGCAGCTCG	GGCTCTTCAT	900
GGCCGTCATG	CCGACTCTCA	TACAGGCGGG	CGCCAGTGCA	TCTTCTAGCA	TTGTCGTGGA	960
AGTTCTCCGA	ATCCTGGTTT	TGATTGGTCA	GATTCTTTTT	TCTAGTCGG	CGGTTTTTCT	1020
TTTATGTCTT	GTTATAAAGA	AGTATCTCAT	TGGACCCTAT	TATCGGAAGC	TGCACATGGA	1080
AAGCAAGGGG	AACAAAGAAA	TCCTGATCTT	GGGAATATCT	GCCTTTATCT	TCTTAATGTT	1140
AACGGTCACG	GAGCTGCTGG	ACGTCTCCAT	GGAGCTGGGC	TGTTTCCTGG	CTGGAGCGCT	1200
CGTCTCCTCT	CAGGGCCCCG	TGGTCACCGA	GGAGATCGCC	ACCTCCATCG	AACCCATCCG	1260
CGACTTCCTG	GCCATCGTTT	TCTTCGCCTC	CATAGGGCTC	CACGTGTTCC	CCACGTTTGT	1320
GGCGTACGAG	CTCACGGTGC	TGGTGTTCTT	CACCTTGTC	GTGGTGGTGA	TGAAGTTTCT	1380
CCTGGCGGCG	CTGGTCCTGT	CTCTCATTCT	GCCGAGGAGC	AGCCAGTACA	TCAAGTGGAT	1440
CGTCTCTGCG	GGGCTTGCCC	AGGTCAGCGA	GTTTTCTTTT	GTCCTGGGGA	GCCGGGCGCG	1500
AAGAGCGGGC	GTCATCTCTC	GGGAGGTGTA	CCTCCTTATA	CTGAGTGTGA	CCACGCTCAG	1560
CCTCTTGCTC	GCCCCGGTGC	TGTGGAGAGC	TGCAATCACG	AGGTGTGTGC	CCAGACCGGA	1620
GAGACGGTCC	AGCCTCTGAT	GGCTCGGAGA	TGATGGACCG	TGGAAGGGAA	GCGTCTGTGG	1680
GGAGTGAGCG	CTTAGATGGC	CAGCAGCTGC	TCCTTCTGGG	AAGCTCGCAC	CTTGGCAACA	1740
GAACAGCCCT	CTAGCAGAGC	GTCAGTGCAG	TCGTGTTATC	CCGGCTTTTA	CAGAATATTC	1800
TTGTCCTATT	TTAGAATTTT	CCGGAGTAGT	TTATTTGCAG	TCTGTTGATT	ATGTGCAGTA	1860
GACCCGGGAC	ACTGCGTTTT	ACCGATCACC	TTGAATGTGG	TGCCTGGATG	TGCCTTTTTT	1920
TTTTTTCCCT	GAAATTATTA	TTAATTTTCT	ATKKGAGTT	CATCAGTTCA	TAGTTTTTTT	1980
AGTAAAGAAG	CAAAATTAAA	AGGCTTTTAA	AAATGTACAA	CTTCAGAATT	ATAATCTGTT	2040
AGTCAAATAT	TTGTTATTAA	ACATTTCTGT	AATATGAAGT	TGTAATCCTG	GCCGTGAGCT	2100
TGGAAGCTTA	CTTTTGATT	TTAAAGCCTA	TGTTTTCTAA	AATGAGACAA	ATACGGATGT	2160
CTATTTGCCT	TTTATTGTAA	CTTTTAAATG	AAATAATTTT	ATGTCAATTT	CTATTAGATA	2220
TATCACTTAA	AATATTTGGT	TTTAAATCAC	AAGAATATGT	ATTCTTTAAT	AAAGATAATT	2280
TATGATCATG	GTATAATTAA	TTGAAATTTA	TTAAAATCTG	TTTTTATTAA	AAAAAAAAAA	2340

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Glu Leu Leu Ala Ala Glu Lys His Gln Val Glu Ala Leu Lys Asn
 1              5              10              15

Met Gln His Gln Asn Gln Ser Leu Ser Met Leu Asp Glu Ile Leu Glu
      20              25              30

Asp Val Arg Lys Ala Ala Asp Arg Leu Glu Glu Glu Ile Glu Glu His
      35              40              45

Ala Phe Asp Asp Asn Lys Ser Val Lys Gly Val Asn Phe Glu Ala Val
      50              55              60

Leu Arg Val Glu Glu Glu Glu Ala Asn Ser Lys Gln Asn Ile Thr Lys
      65              70              75              80

Arg Glu Val Glu Asp Asp Leu Gly Leu Ser Met Leu Ile Asp Ser Gln
      85              90              95

Asn Asn Gln Tyr Ile Leu Thr Lys Pro Arg Asp Ser Thr Ile Pro Arg
      100             105             110

Ala Asp His His Phe Ile Lys Asp Ile Val Thr Ile Gly Met Leu Ser
      115             120             125

Leu Pro Cys Gly Trp Leu Cys Thr Ala Ile Gly Leu Pro Thr Met Phe
      130             135             140

Gly Tyr Ile Ile Cys Gly Val Leu Leu Gly Pro Ser Gly Leu Asn Ser
      145             150             155             160

Ile Lys Ser Ile Val Gln Val Glu Thr Leu Gly Glu Phe Gly Val Phe
      165             170             175

Phe Thr Leu Phe Leu Val Gly Leu Glu Phe Ser Pro Glu Lys Leu Arg
      180             185             190

Lys Val Trp Lys Ile Ser Leu Gln Gly Pro Cys Tyr Met Thr Leu Leu
      195             200             205

Met Ile Ala Phe Gly Leu Leu Trp Gly His Leu Leu Arg Ile Lys Pro
      210             215             220

Thr Gln Ser Val Phe Ile Ser Thr Cys Leu Ser Leu Ser Ser Thr Pro

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225		230		235		240
Leu Val Ser Arg Phe Leu Met Gly Ser Ala Arg Gly Asp Lys Glu Gly						
	245			250		255
Asp Ile Asp Tyr Ser Thr Val Leu Leu Gly Met Leu Val Thr Gln Asp						
	260			265		270
Val Gln Leu Gly Leu Phe Met Ala Val Met Pro Thr Leu Ile Gln Ala						
	275			280		285
Gly Ala Ser Ala Ser Ser Ser Ile Val Val Glu Val Leu Arg Ile Leu						
	290			295		300
Val Leu Ile Gly Gln Ile Leu Phe Ser Leu Ala Ala Val Phe Leu Leu						
	305			310		315
Cys Leu Val Ile Lys Lys Tyr Leu Ile Gly Pro Tyr Tyr Arg Lys Leu						
	325			330		335
His Met Glu Ser Lys Gly Asn Lys Glu Ile Leu Ile Leu Gly Ile Ser						
	340			345		350
Ala Phe Ile Phe Leu Met Leu Thr Val Thr Glu Leu Leu Asp Val Ser						
	355			360		365
Met Glu Leu Gly Cys Phe Leu Ala Gly Ala Leu Val Ser Ser Gln Gly						
	370			375		380
Pro Val Val Thr Glu Glu Ile Ala Thr Ser Ile Glu Pro Ile Arg Asp						
	385			390		395
Phe Leu Ala Ile Val Phe Phe Ala Ser Ile Gly Leu His Val Phe Pro						
	405			410		415
Thr Phe Val Ala Tyr Glu Leu Thr Val Leu Val Phe Leu Thr Leu Ser						
	420			425		430
Val Val Val Met Lys Phe Leu Leu Ala Ala Leu Val Leu Ser Leu Ile						
	435			440		445
Leu Pro Arg Ser Ser Gln Tyr Ile Lys Trp Ile Val Ser Ala Gly Leu						
	450			455		460
Ala Gln Val Ser Glu Phe Ser Phe Val Leu Gly Ser Arg Ala Arg Arg						
	465			470		475
Ala Gly Val Ile Ser Arg Glu Val Tyr Leu Leu Ile Leu Ser Val Thr						
	485			490		495
Thr Leu Ser Leu Leu Leu Ala Pro Val Leu Trp Arg Ala Ala Ile Thr						
	500			505		510
Arg Cys Val Pro Arg Pro Glu Arg Arg Ser Ser Leu						
	515			520		

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCAGCCCGG GCCATGCCGC ACGGCTGCTG ACCGCACGCA GGGGCCGGCC CCGAGGACAC	60
ATGCGGCGGC CTTTGCCGCC TCGCCCCTGA CCCTCTGCCC TGTTCCTCCAT GTTGCAATTC	120
TCGTCAAGTTT CTCGGGCGGT GTAGCTGCCG CTGCCACCAG AGCCGGCGGG GCATCGCGCT	180
GCTCATTCAT CCGGCCGCAC TTTCTTTTCC GTTTCACACC ATCCCTTCCC ATTTCTTCT	240
CCCTTTCCCC GCCAGCTTCG CATCCATCTC CCCACCCCG TAACCCCTCC TGCCTCCATC	300
CACCGGGGCT ATTGCCGCAA AAGA	324

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTGAACATT TCAGAAATAC AGAAGTTGAA GCAGCAGCTT ATGCAGGTAG AGCGGGAAAA	60
GGCCATTCTT TTGGCCAACC TACAGGAGTC ACAGACACAG CTGGAACACA CCAAGGGGGC	120
ACTGACGGAG CAGCATGAGC GGGTGCACCG GCTCACAGAG CACGTCAATG CCATGAGGGG	180
CCTGCAAAGC AGCAAGGAGC TCAAGGCTGA GCTGGACGGG GAGAAGGGCC GGGACTCAGG	240
GGAGGAGGCC CATGACTATG AGGTGGACAT CAATGGTTTA GAGATCCTTG AATGCAAATA	300
CAGGGTGGCA GTAAGTGGG TGATTGATCT GAAAGCTGAA ATTAAGGCCT TAAAGGAGAA	360
ATATAATAAA TCTGTAGAAA ACTACACTGA TGAGAAGGCC AAGTATGAGA GTAAAATCCA	420
GATGTATGAT GAGCAGGTGA CAAGCCTTGA GAAGACCACC AAGGAGAGTG GTGAGAAGAT	480
GGCCACATG GAGAAGGAGT TGCAAAGAT GACCAGCATA GCCAACGAAA ATCACAGTAC	540
CCTTAATACG	550

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Gln Val Glu Arg Glu Lys Ala Ile Leu Leu Ala Asn Leu Gln Glu
1           5           10           15

Ser Gln Thr Gln Leu Glu His Thr Lys Gly Ala Leu Thr Glu Gln His
          20           25           30

Glu Arg Val His Arg Leu Thr Glu His Val Asn Ala Met Arg Gly Leu
          35           40           45

Gln Ser Ser Lys Glu Leu Lys Ala Glu Leu Asp Gly Glu Lys Gly Arg
          50           55           60

Asp Ser Gly Glu Glu Ala His Asp Tyr Glu Val Asp Ile Asn Gly Leu
65           70           75           80

Glu Ile Leu Glu Cys Lys Tyr Arg Val Ala Val Thr Glu Val Ile Asp
          85           90           95

Leu Lys Ala Glu Ile Lys Ala Leu Lys Glu Lys Tyr Asn Lys Ser Val
          100          105          110

Glu Asn Tyr Thr Asp Glu Lys Ala Lys Tyr Glu Ser Lys Ile Gln Met
          115          120          125

Tyr Asp Glu Gln Val Thr Ser Leu Glu Lys Thr Thr Lys Glu Ser Gly
          130          135          140

Glu Lys Met Ala His Met Glu Lys Glu Leu Gln Lys Met Thr Ser Ile
145          150          155          160

Ala Asn Glu Asn His Ser Thr Leu Asn Thr
          165          170

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCCATGAGT GAATTCATCC AAGGGCACGG GTTCAGCAAG GAAAAAAGGT TAACCGTGGT

60

TCCACCAGCA AAAAGAGATT GTCAGCAGCC TGTGCTTCCG TACCGCCACA GTGTTACAA	120
CTAGCCGGGA GGCAAGACTG CCCAACTGTC AGTCCTGACA CAGCTCTCCC TGAGGAGCAG	180
CCACATTCCA GCTCCCAGTG CGCCCCTCTC CACTGTCTCT CCAAGCCTCC TCACCCCTAG	240
TCTTCATCTC CTGTGGACAA ACATCTGGGG TGGAAGTTTT GTAGCCACAC ACAGGATACT	300
GCCCAAGATC CAGCGGGTGT TTTCTTCTCG GTTGTTAGAT GTACAATTGG ATTAATGTCC	360
ATCGTTTTGG AAGACGAGAG AAAGTTGAGA AGAACACGAA GCACAGACCC TGATGTGATA	420
AAACATTTTG TGGTTTCTCT GAGTCACAGA TAAACTTCTG CCATCAAATG GCTACAGTTC	480
ATTTAAATTT AAAAAAAAAA AAAAA	505

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGATACTGTA ATAAATAGGA GACAGCTACA GTGATCCAAC TAAACCAACA GGGGATTTTC	60
ATCAGCACTT CCCTGGTGTA ATCATGGTAC AGATTATTAA AGACACGAAT GAATTTAAAA	120
CATTTTTGAC AGCTGCCGGA CACAACTCG CAGTGGTTCA ATTTTCTTCG AAACGGTGTG	180
GTCCCTGCAA AAGGATGTTT CCTGTTTTCC ATGAGCTGGC TGAAACTTGT CACATCAAAA	240
CAATACCCAC ATTTAGATG TTCAAGAAAA GCCAGAAGGT AACCTATTC TCAAGAATCA	300
AAAGAATAAT TTGCTGTTAT AGAAGTGGAT TCATGAGCAA CCTGATTTTT GAGTTTTGTG	360
GAGCCGATGC TAAAAAATTG GAAGCCAAGA CTCAAGAATT AATGTAAGCT GATCTCCAAG	420
GCAAAATACA CTTGTGACAT TTGAAAAGGC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	480
A	481

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Val Gln Ile Ile Lys Asp Thr Asn Glu Phe Lys Thr Phe Leu Thr
1 5 10 15

Ala Ala Gly His Lys Leu Ala Val Val Gln Phe Ser Ser Lys Arg Cys
20 25 30

Gly Pro Cys Lys Arg Met Phe Pro Val Phe His Glu Leu Ala Glu Thr
35 40 45

Cys His Ile Lys Thr Ile Pro Thr Phe Gln Met Phe Lys Lys Ser Gln
50 55 60

Lys Val Thr Leu Phe Ser Arg Ile Lys Arg Ile Ile Cys Cys Tyr Arg
65 70 75 80

Ser Gly Phe Met Ser Asn Leu Ile Phe Glu Phe Cys Gly Ala Asp Ala
85 90 95

Lys Lys Leu Glu Ala Lys Thr Gln Glu Leu Met
100 105

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCAAAGAG GCCTATTCCT GTGTGCAATC AGTACCTTGA AGGCAGAACA TTCTGAATAA	60
AGTTGGAAAA AGAACAGCTT TGCTTTGCAA AGATTGATGA CAGACTGGTT CCTCAGAGGC	120
CTAGGCTACC CGTCACCCCT TTTTCCAGAG CGAGGGCCTG GAATGAAGGC AGTTTATCCT	180
CTGTCCCTGG AGCCTGGGGT TTGCTTTGGC TCCTTGAGGT GGAAGAGACT AAGAGGGCAG	240
CTGCCCAGAG CAGCTGTGTG TACCTGGCTC CTCTCAGGCT TCCTGATCCC TTCCATTGCA	300
CTGCGCCTTA TCCCTCAGCC AGCCAGACAG CCTCCCTGCT CCTGACCAGC AGATACGTTT	360
CGGAGTGGTT GGTGTGGTTT TTGTGATGAG GGCAGCACGT GGTGGCCAAG GTGGCAAGCT	420
GAGTCTCACA GGCTCACTCC CTCGTTGGTT CCCTGTGGGA ATGGTAGGCC AGGCCCARTA	480
AGCCATGCCC CAACACGTCC TCTCCTCCGG AGGAAGGGCC AGCTGCCARC TGARTCAGCA	540
GCTAGTCCAT AGCACAGCCT TATAACTGTA AAGCCAGGCA TTGCCCATGA GCAGAGCTGG	600
AACCAGAGCT TCAGTCAGTA AGAGGGAGGA TTACCTTCAG GAGAAGGCAA GGAAGAAAAC	660
TGGCTGCTAT CTTTATAGTT CCACTGCCCT AACCAAGTGT CCACATTCTA AATGTGTAGT	720

GTCCATCCCT TATGTAATAG TGGTTTCCCG CCCAAAGTGA GACTTTCCTT TTAATTGGAG 780
 AAGGGTATAG AGGTAGTCCA GGTGGGAACG CCAGAAGTGC TGATTGCCCA GCCATTGGGA 840
 CCACCTGTTC TTGCCCCACT ACCCTCTAGT GGGAGGCCAA AGTAAAGGCT GGCTGGTGGG 900
 TGTCTGTGGA TTGAGGATGT GGCAGGGACT GGTCTCCCA CCTCCCTCTG GCCAAAGATG 960
 GGCTTTGCCC GCTGTGTGCC TGTCACCACC CACCAGCAGT CATGCCCTGG GCTTCCCAAA 1020
 TGGAGAGGTA GCAGGCAACG TTTTAAAAA GAAAGAAAAC AGGAAACTGT ATTGTGTCGG 1080
 GGGAGGCGGG AGGGAGATGA GGAAACGGTT TGGATTTTGT GTGTGGGAGG GTATTTTTTTG 1140
 GGGGTAGTTG TCTGTAACCT TCCTAAGTGC TTTTTTTCCT TTTCTTTTTT AAAGTAAGTT 1200
 GCAGGCTTTG GCTTGAAAAA CCCCAGGGGG ATGGGGGGCA GAAACCTGAG GCTGCTGCCC 1260
 TTTATCTGCC TTCACGGTAC TGTCCCCTTC CCCCAGCTCC TCCCTGACCC CATGGGCCAG 1320
 GCCTCAGACC TTCCAGCTAA CCGCTTCCCA TGAGCCACTA CTCTGATGTC AGCCTATAAC 1380
 CAAAGGAGCT GGGGGGTCCA GGCCTGGTGA CCAACCTTTC TCAGCCCACT CAATCAGGGT 1440
 GCTCCCCACC TGCAGGCAGG AGGCAACACC CTATCTGCTA CCATCAGCCC CTTCCAGAGC 1500
 CCATCTGCCC CGCCCAGCCC TGCCCTGCCC AGCCATACCC TGCTCTGCCC CATCTGGGGG 1560
 TGCCCTGCTC AGGGATGGGC TGGCAGGGCT GTACCCAGCC TCCCTGGTAA GCAGAGACTC 1620
 AAGAAACCTC TGGGGTCCTG TTTTCTGGTC GTGTGATCCC AGGGGTGCAC ATGGGCCCCT 1680
 TGGGTGTCTG AACAGAAGGG CATGGGAGGG AGGGCTGCAC CCCTGCAGTC TTA CTCTGCT 1740
 GGTGTAGCGG GCAGMTGCCC ACTCCCACCC CACCCTGCAC CGCGGGCTCC TGAGTCGGCA 1800
 GATTAAGCAT TTTATAAATT GTATTTTAAA TACATGTTTT AAACCTGTCA AAAAAAAAAA 1860
 AAAA 1864

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val	Leu	Pro	Thr	Cys	Arg	Gln	Glu	Ala	Thr	Pro	Tyr	Leu	Leu	Pro	Ser
1				5					10					15	
Ala	Pro	Ser	Arg	Ala	His	Leu	Pro	Arg	Pro	Ala	Leu	Pro	Cys	Pro	Ala
			20					25					30		

Ile Pro Cys Ser Ala Pro Ser Gly Gly Ala Leu Leu Arg Asp Gly Leu
35 40 45

Ala Gly Leu Tyr Pro Ala Ser Leu Val Ser Arg Asp Ser Arg Asn Leu
50 55 60

Trp Gly Pro Val Phe Trp Ser Cys Asp Pro Arg Gly Ala His Gly Pro
65 70 75 80

Leu Gly Cys Leu Asn Arg Arg Ala Trp Glu Gly Gly Leu His Pro Cys
85 90 95

Ser Leu Thr Leu Leu Val
100

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCCCTCGTA CTGATTTCCT TCGTTGCATT TACAACGTCT ACAAAAATGC CAGCACTCCA	60
TCGACATGAA GAAGAGAAAT TCTTCTTAAA TGCCAAAGGC CAGAAAGAAA CTTTACCCAG	120
CATATGGGAC TCACCTACCA AACAACTTTC TGTCGTTGTG CCTTCAAACA ATGAAGAAAA	180
ACGGTTGCCT GTGATGATGG ATGAAGCTCT GAGCTATGTA GAGAAGAGAC AGAAACGAGA	240
TCCTGCGTTC ACTTATGAAG TGATAGTAGT TGATGATGGC AGTAAAGATC AGACCTCAAA	300
GGTAGCTTTT AAATATTGCC AGAAATATGG AAGTGACAAA GTACGTGTGA TAACCCTGGT	360
GAAGAATCGT GGAAAAGGTG GAGCGATTAG AATGGGTATA TTCAGTTCTC GAGGAGAAAA	420
GATCCTTATG GCAGATGCTG ATGGAGCCAC AAAGTTTCCA GATGTTGAGA AATTAGAAAA	480
GGGGCTAAAT GATCTACAGC CTTGGCCTAA TCAAATGGCT ATAGCATGTG GATCTCGAGC	540
TCATTTAGAA AAAGAATCAA TTGCTCAGCG TTCTTACTTC CGTACTCTTC TCATGTATGG	600
GTTCCACTTT CTGGTGTGGT TCCTTTGTGT CAAAGGAATC AGGGACACAC AGTGTGGGTT	660
CAAATTATTT ACTCGAGAAG CAGCTTCACG GACGTTTTCA TCTCTACACG TTGAACGATG	720
GGCATTTGAT GTAGAACTAC TGTACATAGC ACAGTTCTTT AAAATTCCAA TAGCAGAAAT	780
TGCTGTCAAC TGGACAGAAA TTGAAGGTTT TAAATTAGTT CCATTCTGGA GCTGGCTACA	840
AATGGGTAAA GACCTACTTT TTATACGACT TCGATATTTG ACTGGTGCCT GGAGGCTTGA	900

GCAAACTCGG AAAATGAATT AGGTTGTTTG CAGTCTTCAG TTGTGTTCTT ATGCTTCAGT 960
 GTCACATTTT ATTTCATTTG AACTAAAAAT TTTAAGTAAA GCTGAAATAA ACTTCTTGTC 1020
 ATTGTCAAAA AAAAAAAAAA A 1041

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Pro	Ala	Leu	His	Arg	His	Glu	Glu	Glu	Lys	Phe	Phe	Leu	Asn	Ala	1	5	10	15
Lys	Gly	Gln	Lys	Glu	Thr	Leu	Pro	Ser	Ile	Trp	Asp	Ser	Pro	Thr	Lys	20	25	30	
Gln	Leu	Ser	Val	Val	Val	Pro	Ser	Asn	Asn	Glu	Glu	Lys	Arg	Leu	Pro	35	40	45	
Val	Met	Met	Asp	Glu	Ala	Leu	Ser	Tyr	Val	Glu	Lys	Arg	Gln	Lys	Arg	50	55	60	
Asp	Pro	Ala	Phe	Thr	Tyr	Glu	Val	Ile	Val	Val	Asp	Asp	Gly	Ser	Lys	65	70	75	80
Asp	Gln	Thr	Ser	Lys	Val	Ala	Phe	Lys	Tyr	Cys	Gln	Lys	Tyr	Gly	Ser	85	90	95	
Asp	Lys	Val	Arg	Val	Ile	Thr	Leu	Val	Lys	Asn	Arg	Gly	Lys	Gly	Gly	100	105	110	
Ala	Ile	Arg	Met	Gly	Ile	Phe	Ser	Ser	Arg	Gly	Glu	Lys	Ile	Leu	Met	115	120	125	
Ala	Asp	Ala	Asp	Gly	Ala	Thr	Lys	Phe	Pro	Asp	Val	Glu	Lys	Leu	Glu	130	135	140	
Lys	Gly	Leu	Asn	Asp	Leu	Gln	Pro	Trp	Pro	Asn	Gln	Met	Ala	Ile	Ala	145	150	155	160
Cys	Gly	Ser	Arg	Ala	His	Leu	Glu	Lys	Glu	Ser	Ile	Ala	Gln	Arg	Ser	165	170	175	
Tyr	Phe	Arg	Thr	Leu	Leu	Met	Tyr	Gly	Phe	His	Phe	Leu	Val	Trp	Phe	180	185	190	
Leu	Cys	Val	Lys	Gly	Ile	Arg	Asp	Thr	Gln	Cys	Gly	Phe	Lys	Leu	Phe	195	200	205	

Thr Arg Glu Ala Ala Ser Arg Thr Phe Ser Ser Leu His Val Glu Arg
 210 215 220
 Trp Ala Phe Asp Val Glu Leu Leu Tyr Ile Ala Gln Phe Phe Lys Ile
 225 230 235 240
 Pro Ile Ala Glu Ile Ala Val Asn Trp Thr Glu Ile Glu Gly Ser Lys
 245 250 255
 Leu Val Pro Phe Trp Ser Trp Leu Gln Met Gly Lys Asp Leu Leu Phe
 260 265 270
 Ile Arg Leu Arg Tyr Leu Thr Gly Ala Trp Arg Leu Glu Gln Thr Arg
 275 280 285
 Lys Met Asn
 290

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CNCCATCGGG GAACACCAGA AAGAACACT

29

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TNTCTGGCAT ATCCGTCAGG TTAAACTCC

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CNCTGGTTCT ACATCAATAC CAGCTTTCC

29

- (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNACAACAGT GATATTTGAG AGCTTCAAG

29

- (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CNGTAACACC TCTCCAACGC TTTCGATGC

29

- (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNCAAGGACA GACACGTGGA AATGAAGAC

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ANGTCCACCT CATAGTCATG GGCCTCCTC

29

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TNTCAGCCAG CTCATGGAAA ACAGGAAAC

29

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CNTGGGAAGC GGTTAGCTGG AAGGTCTGA

29

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TNTCTTCTTC ATGTCGATGG AGTGCTGGC

29

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Val Lys Val Gln Leu Ala Leu Val Phe Phe Lys Asn Leu Ala Ser
1 5 10 15

Ser Cys Thr Leu Asp Ser Ala Leu Asn Ala Ala Ser Tyr Tyr Asn Phe
20 25 30

Thr Val Leu Lys Val Pro Arg Ser Met Thr Asp Pro Gln Asn Met Glu
35 40 45

Phe Gln Val Pro Val Ile Leu Thr Ser Gln Ala Asn Ala Pro Leu Leu
50 55 60

Ala Gly Asn Thr Cys Gln Asn Val Val Ser Gln Val Thr Tyr Glu Ile
65 70 75 80

Glu Thr Asn Gly Thr Phe Gly Ile Gln Lys Val Ser Val Ser Leu Gly
85 90 95

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTTGTACCAT TCTTGCCAAC TTCTGGGCTG GCAGTATGGA GTCATCTCCC TATCTTTTCAT	60
TGCCTGTGTG AAATCTACTT TCTGAATTCT GCCATTTCCC TCTTCACACT GTCTCCTGGG	120
TTATCTTTGC TTCCTCACAT CCCTATCTCT CTTCCTATAA ACTGGCTCCC GTCACCTCCA	180
TGATCCCTTC AGTGGCTTCT GAGCTGGTCT CCCTGACCCC AAAGCCTCAG CCTTCCAGTC	240
TCCCTACAAA ATCTCAGCAA GTTCATTTTA GGTAAAAATT TGGACATATT TAAAAACGG	300
CTCACCACTT CATGTGAAAA TGATGGCACC CTACCAAGCA GTTTGCAGAG TTACGGTAAC	360
TGTTTCATGC TAATGATGTT ATTCATCCAG TTACAATTTT CTCAAACTC CTTTGGGCAC	420
TCTTTATTTT TAATCAAATT TAAAAGCCAA TATTTTATTT TGAGAATATG AATTAAATTG	480
GGAAATTCAT CCTTGTGGTA CAGTTTACAG ATTTTAAATG TTTACCCATT TATCCTGTTT	540
TTTGATATAT TAATTTCCCA TATAGCTCCA GAGTTATGTG ATATTATTTT TTTGCCAGTA	600
TATTAGAAAA TGATTAATTT CTCATGACCA ACTTCTGAAA AGAAAGACCC AATGCAAAAT	660
GCAATCTATT ACAATTATTT TTTTGAATAA AAAAGAATAT ATTATAGTTC TTTAACATTT	720
GATATTTTAA ATTTGACATA TTCTTGATAT TTGTAAGAAA TTTCCACTGA ATGAATTTTA	780
CACAATTCAG ATACTACCAA TTAACATAATT CTAGCCTAAA CAAATAACAT TATTTTAA	840
TAACAAAATC TTTAAAAATA ATTTTCTATT TTGAACTTTT AGCCATAATG TAAGAAAATA	900
AAATTTTCTA GCAGAATAAT CAAAGAGTGA AACAAAGTTC CAACATGTTT TTTCTTTGCA	960
ATTAAACATG GCACTTTAC AGTTATTTAT TATTCATATC AGTGCACTTA CCGACTTCAT	1020
ATTTTCAAAT CAAAATACAG TGTFTTTCTC CAGTGAAATC CTTATTCTCA TGAATGATAG	1080
AAAACATTGC CAATTTTGAT ATTTCCAGAG TTAATGTTAA ATTATTTGAA AGAAAATTAT	1140
TTAAAATAAT AAAAATAGAC ATTTCAAGAC TATTTCTTAT CACATAATTC AAAAAGTACT	1200
TGGATCAAAT CCTACAGAGT TTCTCCACTA AAATTCTACT TGTGCAGAGG GCATTGAAAC	1260
GCATGAAAAT CAACAGCAGC TTAGTTAGGT TAATTAATTC GGTTAATTAA GCACCTACTA	1320
CATGCTCAGC TCTATGCTAG GTGTCATGAG GAATTAAAAG GACATGTAAT GCACATTTTC	1380
TGATTTCAAG GAGCTTTAAA TATTATTGTG TAGAAAAAGT TAACATCTAT GAAAATAGAA	1440
GTGGGGCAAT TTTGTGCTTA ATTCCATGGT CCAGATACAT CAAAAAATCA ATGTGGGCTG	1500

TCAAAGAAGG TTTCTTGATA GTCATGAGTC AGCCTGATTC TTGAAAGGAT ATGTGGAATA 1560
TAAAATTTTA TTTATATTCC TTTTGAGAAA ATACTGAGAA AACCATCTTC CCTGGAAAAG 1620
AGAACGTATT GTAAAGAAAAG TACATGAAAT TGAAGGTTGA ATATCCAACA TCCCCACAC 1680
TGCCCCAGTG TCTCTGCTCC CTTACTGAGC CTTACTATTA TTCTTCATAG CCCTATCACT 1740
ACCTAGTCTA GTATTCACTG AACTGTGTCA TCCACTAGAA TATGAGCATA ATGAGAGCAG 1800
AGACTACACC TGTCGGTTCA GTATTCTATC CTCAGCACAT AGAATGGTAC CTGGCACATA 1860
GCAGATGCTA AAATAAAATT TAAATGAATA AATTAATTCA ATCAACAAC TCAAGGTGTT 1920
ATTATTACCT ACAACTATTG TTTACAAGAG GTATGCACCG TGGAAGATCC TGGAGACACA 1980
ACAATGAATA AAGCCAAGCC AGTTCCTGCC CCCGTGGAGC TTGTAGTCAA GACATTGAAC 2040
AAGTGATCAG AAAGATGTTG ACTGCTGCAG CAGAGGGTTG CAAGCTGCTC ATGAGTATAT 2100
AACAAGTAGC CCTAACCAAA GCATTCTCTC CCTTGGTTTA ATGTCCACCC ATTGAGGTGA 2160
CTGCTAAATA CTAATCCATG ACTCTATCCC TTGGCATTCA AACTCACACA TCCACTTACC 2220
TGCCTCTCCA ACCTCATCTC CCTCCACTCA CAAGAGCCCA TCATATTATT CATCAAAATG 2280
AAACTGCACC CAGTTCTTCT GAACATATTA CCTTACAAAA CTTTCATTTA TGCCTGGTGA 2340
CTCTCATCAG GCATTCAAAA GCTTTCCCTC AGTGCTTCAG GGCTCTTCCT TTTCTTCCCT 2400
TTATACATAC ACCTTTATGT ATCTTCATAC GTACCCTGCA TAACCTCATA TATCTTAGCA 2460
TTTACCATAT TCTGTTGAAA AACTGTTTCC ATTTCTCTTT ACTTACTAGA ATGTAAACAG 2520
ATGCACAATG TTGAGAAAAT GAAAAGTGAC AACTTTGTTT ACAAGTTTAG AAATTATCAG 2580
ATTCTCACYT AAGCTCTAGT CTCTGTAAAG TCCACAAC TAATAATAA GTGAAGAAAA 2640
ATGTTAACAG AGAGGGAGGA ATCAAAAACA AAGAACTATT TAAAAA AAAA 2696

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Thr Leu Ser Leu Gly Ile Gln Thr His Thr Ser Thr Tyr Leu Pro
1 5 10 15
Leu Gln Pro His Leu Pro Pro Leu Thr Arg Ala His His Ile Ile His
20 25 30

Gln	Asn	Glu	Thr	Ala	Pro	Ser	Ser	Ser	Glu	His	Ile	Thr	Leu	Gln	Asn
	35					40						45			
Phe	His	Leu	Cys	Leu	Val	Thr	Leu	Ile	Arg	His	Ser	Lys	Ala	Phe	Pro
	50					55					60				
Gln	Cys	Phe	Arg	Ala	Leu	Pro	Phe	Leu	Pro	Phe	Ile	His	Thr	Pro	Leu
65					70					75				80	
Cys	Ile	Phe	Ile	Arg	Thr	Leu	His	Asn	Leu	Ile	Tyr	Leu	Ser	Ile	Tyr
			85					90					95		
His	Ile	Leu	Leu	Lys	Asn	Cys	Phe	His	Phe	Ser	Leu	Leu	Thr	Arg	Met
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CGCGCTAACT	GTGCTCCTCC	GGGGCCCTCC	GCCTGCTCCC	AGCCATGGTG	GCCTGGCGCT	60
CGGCGTTCCT	TGTCTGCCTC	GCTTTCTCCT	TGGCCACCCT	GGTCCAGCGA	GGATCTGGGG	120
ACTTTGATGA	TTTTAACCTG	GAGGATGCAG	TGAAAGAAAC	TTCCTCAGTA	AAGCGATCAC	180
TGTAAGGATG	ACATGGGAGG	AGCCATGTGA	AGCACTCAGC	ACAGTCCTTG	GAACAAGAGC	240
CATGGGACCA	CACCACCACC	ACCACAACCA	ATAGGCCAGG	AACCACCAGA	GCTCCGGCAA	300
AACCTCCAGG	TAGTGGATTG	GACTTGGCTG	ATGCTTTGGA	TGATCAAGAT	GATGGCCGCA	360
GGAAACCGGG	TATAGGAGGA	AGAGAGAGAT	GGAACCATGT	AACCACCACG	ACCAAGAGGC	420
CAGTAACCAC	CAGAGCTCCA	GCAAATACTT	TAGGAAATGA	TTTTGACTTG	GCTGATGCCC	480
TGGATGATCG	AAATGATCGA	GATGATGGCC	GCAGGAAACC	AATTGCTGGA	GGAGGAGGTT	540
TTTCAGACAA	GGATCTTGAA	GACATAGTAG	GGGGTGGAGA	ATACAAACCT	GACAAGGGTA	600
AAGGTGATGG	CCGGTACGGC	AGCAATGACG	ACCCTGGATC	TGGCATGGTG	GCAGAGCCTG	660
GCACCATTGC	CGGGGTGGCC	AGCGCCCTGG	CCATGGCCCT	CATCGGTGCC	GTCTCCAGCT	720
ACATCTCCTA	CCAGCAGAAG	AAGTTCTGCT	TCAGCATTCA	GCAGGGTCTC	AACGCAGACT	780
ACGTGAAGGG	AGAGAACCTG	GAAGCCGTGG	TATGTGAGGA	ACCCAAGTG	AAATACTCCA	840
CGTTGCACAC	GCAGTCTGCA	GAGCCGCCGC	CGCCGCCCGA	ACCAGCCCGG	ATCTGAGGGC	900

CCTGTCCAGC	TGCAGGCATG	CACAATGGTG	CCACCGCTTG	TCACCCGGCT	CCCCCACCC	960
CTTCATTTGG	ACCCGCAGCT	GCTGTGCTGC	TCTGTGCCGT	CGGCTCCTTG	TTGGTCTGAG	1020
TTTCCCGGAT	GAGCTCTGGG	TGTTTGTGAG	TTTGGTTTCT	CTGCCCTGCC	CCAAGCGTGC	1080
TGAGACTTGG	TGCCGAAATT	CAAGAGCCAG	CTCTGATAGA	AAGCCAGCAC	CAGCCTCGGG	1140
AGCTGCTGAG	CCACCAACTC	CCAAAGCCAG	CCTGCCTCCA	GCTTTACTGA	GCACAGGATG	1200
CGGGGGCCAA	GATGATGCTG	AGGCCTGATG	ACATTTATGC	TTAGGGGACA	AGAGTTTGAA	1260
CTCAAGGGAC	TGTGACCCCT	GCACACTGGA	GTGGCTCATT	GTGGCAGGTT	TCTGCCAATA	1320
GACAGCCCCT	GACAGTGGCC	TCAAGGAGCT	GCAGGTGGGG	GGCTCAGCCT	GCACCCACTT	1380
GGAGCCCCTG	CAAGGAGCGA	ACCGGTCAGC	ACCAAGTAAC	ACCACACACA	CGCAGCACCC	1440
AGGATGATGG	TTTCACTTCA	GTCTTCCCCA	TCCCAGGTTT	TATGTTGCTG	GGCTTCCGGA	1500
GAGCCGGTCC	AAGCGGAGGC	TTTCAGTGAT	TTAAGTACAA	ACATGCATCT	CGTGATAGTC	1560
CTGCCTTGAG	AGCTTAGGAA	TCTTCCGGAT	AAGTATGAAG	CAATTCGTAG	GCCTGTTTCC	1620
CATCTGATTC	CATAGGGGGC	TGGGTGTGGC	TTCGGGTTGA	CATGAGAAAG	GTCTTTAGCA	1680
ATCATTTCTG	CACCGGAGAT	GAGTTTTATC	CTGTGTTGGG	GAGAGGTGCT	CACCCTCCAC	1740
CCTGTGTCCC	TGTTTTGGTA	GCAAGAGTGA	CCGATGTCAA	GAACGAGCAT	CAAAGCCAGA	1800
ATCCTGCTTG	TTTGCTTAAA	AATGTAATTG	GGGGCGGCGG	GGGAGGAGAG	GGGAAAGAGA	1860
CATTCGCTTG	GTTTAGTGAA	ACGCAGGTGA	CTTTGTAGCT	CTGTGGTCAG	CCTACTTGTC	1920
TGCTCTGAGG	GAGAGTGCCT	GGGGAGCCAT	GCTCACCGTG	GCAAACACAG	GAACCCCATG	1980
ACTCGCCCCCT	CACCTGGCGT	GGAGCTGCCT	GGTTTGGGCT	GGAGCAGAGC	TGGTTTCCTG	2040
GAATGTTCCCT	TTGGCCCACA	TATGGTTCTG	TCCCGGTGAG	CTCTGTTGTC	AGAGGCTCAC	2100
GGGACAGAAC	CACATGCTAG	GGTCTAGGGC	CCCTGTCTAC	TGATAGTCAG	TTTGCTGTGT	2160
CAGAAAGCAC	TTCTGAAAGC	AGATATGAGT	CACCAGACAG	GCAGGATCTT	ACAAAACCTCA	2220
CGGGCCTCTT	TGGTCTGCAT	GATGGCCCCA	TGCGTTTCAT	AGGCTGTCCA	CTGAGCGGGA	2280
TTGTCTGCTG	AGTGGGATGA	GCCAACTCCA	GTTTCTTAAG	GAAACCACTG	GAATCTGCAG	2340
CCCCCACATG	CATCTGTCTA	ACGCATGCCT	CGTGTTTCGTT	TTGCAAACAT	GCCTGTGGTG	2400
GAGGGTGGTC	AGTTGTAGCC	CTGTGCGTCT	CAAGGCTGCC	TTGTGAGGCC	ATTCCCAGTG	2460
CGTGCCCTTG	AGCTCCTTAC	CACCCCTTTT	CCTGCTCGGC	CCTTTAATCC	CTGACAGACC	2520
TGGA CTGTGT	GGCTGAAGGG	GGACCTGCAG	CACTGCAGAA	ATGCCTCTGC	GTGGTGCCAT	2580

GAAGGAAAGA AACCTTGGCC TGGTCTCGAG AAGCTTCCCA TGCTTCAGGA AGTTAGTAAG 2640

GGTGGGGTGG CTTGCAGGAT TGGCCTGTTT CCAGGGCCTC CCACACTCAT TGGCCAGATT 2700

GTGAACTTTG TCAGGCTTGT CCCTCCCTGA TACCAAGTAT GTCGAGAACC GATGGCCCCA 2760

CCCTCTGGCT GGTGCTGGGC CGGAGGTGGC TATGGAGGAT TTTGGCATGC GTGGCCTGTC 2820

GCCACCTGGA CAGCGTGACC TCAGGGGTTG TCCACTTTAC CTTTATGGTG AGGCCTGTCTG 2880

GATGGCTAAG TCCTTGAAAC CCTAGAGCTG TGACGTAGAA TATGTGCTGT CTGTGAGACC 2940

GTGTTCCAG GAGCACTGAC TGCAGTTGAG AGAGACCCAT TTTGCTCTCC CTTACCGCCC 3000

CCCCCCCCGG GTGCTTTCTG CACAAAGCCT AGAGCCTGGC ACTCAAGCCC ACCGGTGGCA 3060

GCTCCTAGTG ACTGGACATG CCTGGAAGAC CCCTCAGCCT TCTGTTTGCA GAACGTTTAT 3120

TTCAGGAGCT TCTCCTTCCC ACAGACATCT TACACTTGCT CGACACTGCC ACCTGCAGAA 3180

GCCTGGCGGG CTCTGGTCAC CATGTGTCTA TCTGAAGGTT GCACTGGCCA GCATGGGCCT 3240

GTCCAAGCG AGAGGGGAGA CACAGTGGAC TGAAAGGACT GGTTGAAAGT GGCCAATCTC 3300

TGTCAGCTTA ATTTGGCAGA GAAAATTTGT AACAACTCTG AGCACATGCT GGGTGAAGTC 3360

ACAGCTCAAG GAAAGATAAA GCTGGGCGGA AGGAGGTGTG CGTGGCTTCT GGGGTGGGAC 3420

CCAGAGGGGA GGCTCTGGGA CAGGGGCTGG GGTTCAGTGC CAGGGCCCTG AGGAAGAAAT 3480

GGGGACTGAT CTCAAAATTC CAGAATTCCC TGTACATCTG TTCACGTGCT TGTGTCCAGG 3540

TGTGACTTGT AAAGTGTCTA GTGTTTGCAT TAAATAAAAT GGCACCGAGC AAAAAAAAAA 3600

AAAAAAAAAA AAAA 3614

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Val	Lys	His	Ser	Ala	Gln	Ser	Leu	Glu	Gln	Glu	Pro	Trp	Asp	His	Thr
1				5					10					15	
Thr	Thr	Thr	Thr	Thr	Asn	Arg	Pro	Gly	Thr	Thr	Arg	Ala	Pro	Ala	Lys
			20					25				30			
Pro	Pro	Gly	Ser	Gly	Leu	Asp	Leu	Ala	Asp	Ala	Leu	Asp	Asp	Gln	Asp
		35					40					45			

Asp Gly Arg Arg Lys Pro Gly Ile Gly Gly Arg Glu Arg Trp Asn His
 50 55 60
 Val Thr Thr Thr Thr Lys Arg Pro Val Thr Thr Arg Ala Pro Ala Asn
 65 70 75 80
 Thr Leu Gly Asn Asp Phe Asp Leu Ala Asp Ala Leu Asp Asp Arg Asn
 85 90 95
 Asp Arg Asp Asp Gly Arg Arg Lys Pro Ile Ala Gly Gly Gly Gly Phe
 100 105 110
 Ser Asp Lys Asp Leu Glu Asp Ile Val Gly Gly Gly Glu Tyr Lys Pro
 115 120 125
 Asp Lys Gly Lys Gly Asp Gly Arg Tyr Gly Ser Asn Asp Asp Pro Gly
 130 135 140
 Ser Gly Met Val Ala Glu Pro Gly Thr Ile Ala Gly Val Ala Ser Ala
 145 150 155 160
 Leu Ala Met Ala Leu Ile Gly Ala Val Ser Ser Tyr Ile Ser Tyr Gln
 165 170 175
 Gln Lys Lys Phe Cys Phe Ser Ile Gln Gln Gly Leu Asn Ala Asp Tyr
 180 185 190
 Val Lys Gly Glu Asn Leu Glu Ala Val Val Cys Glu Glu Pro Gln Val
 195 200 205
 Lys Tyr Ser Thr Leu His Thr Gln Ser Ala Glu Pro Pro Pro Pro Pro
 210 215 220
 Glu Pro Ala Arg Ile
 225

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1077 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AATCGGGAGT CCCAACAGCG TTAGGTTTTT TTTTTTGTTT GTTTGTTTGT TTTGTTTTTT	60
TCCAACCCTC TTTCGGATGG ACGGGGGAAA GAGAGAAAGA AAAACGAGGG AAAATCAACA	120
AAATGTGCGA TGCAAAGAGT CGATTTTCGC GGGGTTTGTC AACTTCGCCA CTGCCGCACG	180
CGAATCGACG TCGTCACGTG ACGGTCTGCC TCCGCCCTTA TTA ACTCTCA GCCCAGCGGC	240
GGTTTCCAGG ACCTCAGACT TTTTGCCGAG GCGGCAGTCC CTAGACGAAG CGAAGGAGGC	300


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GGCGCCTGCC CCGCCCACAA GAGCTGCCGC GCGCGGGTGT TATAGCTCCA CCCCATCTGC      360
AAAGGAAGGG GGAGCGGAAA GAGCGGGATC TAGCGTGGGA TAAAAGTGGG ACTACTACAG      420
TGTAAGTGGG CATGCGCCCC TCCTAGAAAT GATGGGAATG CAAAAGCCCT TGACTGCTCC      480
AGGACTCGAG GGATCCTCGG TGCCAGGATG CTGGGTCAAG CGCTCCGCCG GGACAGAGGA      540
CTCATACCAG GGAAATGGAG CCCAGCCTCG TGATAAACTA CGACCCAAGC TGGGGGAGGA      600
ACCTAGTTTT CGAAAGGAAA ATAATATGCG CAAGCTTTAA CTGAGCAGTG GGATGGTCTT      660
AAATACCAAA GGAATGACTT TAAATCTTGC TGGATGGGAC TGCCACTCAC CGCTAGAAAT      720
CGGGGATCAA CAGCAAATC TGGATGACCC TGTAACCACA TCTCCAGTTC AGCCCGGCGA      780
GGGGCATCCT CACCCACCAG CAAAGTACCA TCCACCTTAT TGATGACAGG GATCCGGGTC      840
TCCAGGTCCA CATCAAGGTG ATTAGGCTCT TCCATGCACT CCACCTCCAG CTGCAAACCC      900
AGAATCCACC CCCATGAGCA CATACTCTTC TTTGGGGGAG GGAGGGAGGG GGAGCAGGGC      960
CAATGGTAGT CATGAAATGA CTCTAGTATT TTCCATTCCC CCAGTCCCAC TGCCTTCATC    1020
AATTATTGGG AATAAAAAGA CAATCTAATC GTCAAAAAAA AAAAAAAAAA AAAAAAA      1077

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(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Met Asp Gly Gly Lys Arg Glu Arg Lys Thr Arg Glu Asn Gln Gln Asn
1              5              10              15

Val Arg Cys Lys Glu Ser Ile Phe Ala Gly Phe Val Asn Phe Ala Thr
20              25              30

Ala Ala Arg Glu Ser Thr Ser Ser Arg Asp Gly Leu Pro Pro Pro Leu
35              40              45

Leu Thr Leu Ser Pro Ala Ala Val Ser Arg Thr Ser Asp Phe Leu Pro
50              55              60

Arg Arg Gln Ser Leu Asp Glu Ala Lys Glu Ala Ala Pro Ala Pro Pro
65              70              75              80

Thr Arg Ala Ala Ala Arg Gly Cys Tyr Ser Ser Thr Pro Ser Ala Lys
85              90              95

Glu Gly Gly Ala Glu Arg Ala Gly Ser Ser Val Gly

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(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

TAAGAATTAA AAATGTCATC CAAACAAGAA ATAATGAGTG ACCAGCGGTT TAGACGGGTT      60
GCAAAGGACC CGAGATTTTG GGAAATGCCA GAAAAGGATC GAAAAGTCAA AATTGACAAG      120

AGATTTTCGAG CCATGTTTCA TGACAAGAAG TTCAAGTTGA ACTATGCCGT GGATAAAAGA      180

GGGCGCCCCA TTAGCCATAG CACTACAGAG GATTTGAAGC GTTTTACGA CCTTTCAGAT      240

TCTGATTCCA ATCTCTCTGG TGAAGATAGC AAAGCATTGA GTCAAAAGAA AATAAAGAAG      300

AAAAAAACCC AGACTAAAAA AGAAATCGAT TCAAAAAATC TAGTTGAGAA AAAGAAAGAA      360

ACCAAGAAGG CTAATCACAA GGGTTCTGAA AATAAACTG ATTTAGATAA TTCTATAGGA      420

ATTAAAAAAA TGAAACCTC ATGTAAATTT AAGATAGATT CAAACATAAG TCCGAAGAAG      480

GATAGCAAAG AATTTACACA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      540

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA      588

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(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Met Ser Ser Lys Gln Glu Ile Met Ser Asp Gln Arg Phe Arg Arg Val
1           5           10          15

Ala Lys Asp Pro Arg Phe Trp Glu Met Pro Glu Lys Asp Arg Lys Val
20          25          30

Lys Ile Asp Lys Arg Phe Arg Ala Met Phe His Asp Lys Lys Phe Lys
35          40          45

Leu Asn Tyr Ala Val Asp Lys Arg Gly Arg Pro Ile Ser His Ser Thr
50          55          60

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Thr Glu Asp Leu Lys Arg Phe Tyr Asp Leu Ser Asp Ser Asp Ser Asn
 65 70 75 80
 Leu Ser Gly Glu Asp Ser Lys Ala Leu Ser Gln Lys Lys Ile Lys Lys
 85 90 95
 Lys Lys Thr Gln Thr Lys Lys Glu Ile Asp Ser Lys Asn Leu Val Glu
 100 105 110
 Lys Lys Lys Glu Thr Lys Lys Ala Asn His Lys Gly Ser Glu Asn Lys
 115 120 125
 Thr Asp Leu Asp Asn Ser Ile Gly Ile Lys Lys Met Lys Thr Ser Cys
 130 135 140
 Lys Phe Lys Ile Asp Ser Asn Ile Ser Pro Lys Lys Asp Ser Lys Glu
 145 150 155 160
 Phe Thr Gln

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTATATTTTG GTTTACTTAC TCCTCTATTT CAGAAATTGA AAAAGATCCC CAAGGATCTG 60
 TTACTACTGC ATTTCTTCT TGCTCTGTCT ACAGCCTAGG CCAACTAGTC AGGGTCTGGA 120
 CATGCATCTC CTAAAGGAAG AACTGTGTAG CACCATTGAT CACAATGTAA CATTTCCATG 180
 CTGCATTAAG GGTGTCTCTC TCTAATCATG ATTGTACCTG TCTCTTCCTG GGTAAGGGA 240
 GATTTTTTTTT TTTTAATGTG TAAAGAATTG ATGCSAGCCA GGAACATGTC TGTAGTCCCA 300
 GCTACTTGGG CACACGCCTG TAGTCCMSCG CCACTCGAGC ACACACCTGT AGTACCAGCT 360
 ACTCTGGAGG CTGAGGCAGG AGGATCACTT GAGCCCAGGA GATTAAGACT GTAGTATACT 420
 ATGATCGTGC CTGTGGCTAG CCACTGTGCT CCAGCCTGGG CAACACCATC GTAAAAATAA 480
 ATAAATAAAT AAATAAATTG GGGAGGACAG CCTCACTGGT ATCAGACTTA CAGGACCAGA 540
 TAGACAAGAT GGGTATAAGG GGAGCTGAAG TCTGTGTTCA TATGAGGAAG AGAAGACCAA 600
 GCCCTGGGAC TTTGGCTGAA TTCCTCCGTG GGGCTGGACG GCAGTGATCT CCTGTTCCCT 660
 ATGTGTAAAC AAAGATTCCA GGGCGTGGTT TTGCACTCCT GTTGTACTCT TTTAGAGGTG 720

GAAAAGAGGT GGATACTGAG ATCTAAGAGG AAAGGATAGT CATTCACGTT CTGAGATATG	780
CGCTCTCTCT ATTGTTCTCTG WACACAAAGG GATAGTCTCT TTTCTGGAGC TGATGTCCCT	840
GCTTGGAGGT TAGCCCCAAA ACATGGCTCT TGTATTGTTC TAAGAGAAAA GGCTTTCATT	900
TTGGTTCTTC TGATTGGTGT TACCTACTGC CTAATATGTG TTCATTTTTT GACAGAGAGG	960
CAGACTATTG AAAAAGTCTG TGTGAACAGA GAGCAGTTCA TTAAGCCCAT TGCTTTCAGT	1020
AATGTGGCCT TGACCCCTTC TGCTTCCCCC TTCTCCCATG GAGCATGGCA GGGCTTGGTT	1080
ATTTAGAGTC CATACTGCA AGCCATTGAG AGACTTGTTT GCTCAAATGC AAGTTTGCTC	1140
AAAAACAGGT CCTGAAGGCT TGCTTAGGAT TACAGGGATG CTGGGTAAGA ACACCGTTCC	1200
TCTCTCTCGC TGGAGAAATC CCTGTTTCTC TGAATCCCTT TGTGATCCTC ACAGTAATGT	1260
ATTCTGTGCC ACTGTAGGAC ACAAGGCTCT GGGCCAGTAG AACAGGCAGA GAGGTGACAC	1320
TGGGCAGCAA GCTGAGAGCT CTTTCTAAAT GGAGTGAAGG AATTCAGTGG CCTAGTTTCG	1380
CCATTCTCTA ATGAGAAACC AAGGCCAGGC TGAAAAGTGC AATTAGATGT GGTGGATTGT	1440
GGTAACGGCC TCCAGATAAA GGGGTTATCC CTGTGGAAGT GACTTTTCCC CATTTGATCC	1500
CTTTTCAACT CTAAATGGCC AGGCCAGAG CAGAAGAAGG GTTGGGTCTG GAAGGAAGGC	1560
TCCAAAGGAT GAAAGCTTCT CCCTGATCAT AAGGAAGTGC ATCTTTATAG AATTGTTGTG	1620
CATAATGTCA GTAAATCCCT CTCACTTGAC AAGGGACTGG ATTCATCTTG CCTTGAGACG	1680
GGCCAGTAGT TATCAGTGAG TCAAAGCAAA GTGAAAGTTT CAGGAGATGG GACCAATGGT	1740
GCAATGCTCG CCATAACAAA ATTCCTTAAA AATAAAAAAG CTAATGTTAT AGCAACAAAA	1800
AAAGACTGAA GCAAAACCAC ACTGAAATGC ATCCCACTCC AGGAGAGGAA TTCTTAGCGT	1860
AACACTCTAA ATAAATGGAA GGAATCATCA CCTTCCTTAT TTTACCCCTG CCTTGTTTAC	1920
CAGGCTGCCC AGTGCTTACC ATGCAGAAAG CAGTCAGCTG TACTCTGGAA GTTTCTGTTC	1980
TTCTTTCCTG GGGCTTAGGA TATTCTGGGA GCTGTCTGAG CCTTGTGCCT AAGGCTTATC	2040
AGGTGATATA ATCTTCCTGT TCTGGGCTGC TTGCTGGAGG AATAGGAAGT GACATTTATA	2100
AGACACAGGC GGTGTGAGCA TCCATGTGTG GTCTTGGTCT AAACCAGCTC TTGAACAGGT	2160
TAAAGCAAAC AGCAATAACA AAACAAAAAC TACTGATGCT GAGCGTTTTG ATCCTAGTAA	2220
TATTTCAAAT ATTGTCCTTC TGCATATGTT CTATCCATAT TTGATTCCAA TATACATTAT	2280
TAAGCTTTCT TGGGTACTAT TTTGCTGGGG CTCTTGCGTG AAGGTGGTAC CTGTCTCATG	2340
ATCCTTAAAA GAGAGAGGCT TTTTTCATCC AAAGCTGTAG TGTTGGGAAC TGGGGTGGGA	2400
GAGGCACTTT TTGGAATTCT GAAAGAATCA TATCTGTGTA TATACATACT GAGTGGGGAA	2460

GGATGGGGGT TGGCAGGGGT TGAGGGAGGT GGAACAAAC AGTGAGTATG GGAACAGGCA 2520
 GTCACCTCGA GTGTGGGAGG TCACCTGGGT CCGTCGTCTT CCTTCTGTAT GGTGTTGGGT 2580
 TTATGTACAC ACTATAACAC TTCCTGTGTG AGTTCATGTA CCTGTCTGTG AGTGCTTTGG 2640
 TGTATTGAGC CTCAGTACAC TCCAAGGGCA TTAAAGTCAA GAACTAGAAC CTGGAAAAAA 2700
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
 AAAAAAAAAA AAA 2773

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Arg	Ser	Leu	Tyr	Cys	Ser	Arg	Thr	Gln	Arg	Asp	Ser	Leu	Phe	Ser	1	5	10	15
Gly	Ala	Asp	Val	Pro	Ala	Trp	Arg	Leu	Ala	Pro	Lys	His	Gly	Ser	Cys	20	25	30	
Ile	Val	Leu	Arg	Glu	Lys	Ala	Phe	Ile	Leu	Val	Leu	Leu	Ile	Gly	Val	35	40	45	
Thr	Tyr	Cys	Leu	Ile	Cys	Val	His	Phe	Leu	Thr	Glu	Arg	Gln	Thr	Ile	50	55	60	
Glu	Lys	Val	Cys	Val	Asn	Arg	Glu	Gln	Phe	Ile	Lys	Pro	Ile	Ala	Phe	65	70	75	80
Ser	Asn	Val	Ala	Leu	Thr	Pro	Ser	Ala	Ser	Pro	Phe	Ser	His	Gly	Ala	85	90	95	
Trp	Gln	Gly	Leu	Val	Ile											100			

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGAAACATTA TGGATCTGTG GAGCTGCTTA TTTCCAGTGA TGCTGATGGA GCCATCCAAA	60
GGGCTGGAAG ATTCAGAGTG GAAAATGGCT CTTCAGATGA GAATGCAACT GCCCTGCCTG	120
GTACTTGGCG AAGAACAGAC GTGCACTTAG AGAACCCAGA ATACCACACC AGATGGTATT	180
TCAAATATTT TTTAGGACAA GTCCATCAGA ACTACATTGG AAACGATGCC GAGAAGAGCC	240
CTTCTTCTTT GTCCGTGACC CTTTCTGACC AAAACAATCA ACGTGTCCCT CAATACCGTG	300
CAATTCTTTG GAGAAAAACA GGTACCCAGA AAATATGCCT TCCCTACAGT CCCACAAAAA	360
CTCTTTCTGT GAAGTCCATC TTAAGTGCCA TGAATCTGGA CAAATTTGAG AAAGGCCCCA	420
GGGAAATTTT TCATCCTGAA ATACAAAAGG ACTTGCTGGT TCTTGAAGAA CAAGAGGGCT	480
CTGTGAATTT CAAGTTTGGG GTTCTTTTTG CCAAAGATGG GCAGCTCACT GATGATGAGA	540
TGTTTCAGCAA TGAAATTGGA AGCGAGCCTT TTCAAAAATT TTAAATCTT CTGGGTGACA	600
CAATCACTCT AAAGGGCTGG ACGGGCTACC GTGGCGGTCT GGATACCAA AATGATACCA	660
CAGGGATACA TTCAGTTTAT ACTGTGTACC AAGGGCATGA GATCATGTTT CATGTTTCCA	720
CCATGTTGCC ATATTCCAAA GAGAACAAAC AGCAGGTGGA AAGGAAACGC CACATTGGAA	780
ACGATATCGT CACCATTGTG TTCCAAGAAG GAGAGGAATC TTCTCCTGCC TTTAAGCCTT	840
CCATGATCCG CTCCCACCTT ACACATATTT TTGCCTTAGT GAGATACAAT CAACAAAATG	900
ACAATTACAG GCTGAAAATA TTTTCAGAAG AGAGCGTACC ACTCTTTGGC CCTCCCTTGC	960
CAACTCCACC AGTGTTTACA GACCACCAGG AATTCAGGGA CTTTTTGCTA GTGAAATTAA	1020
TTAATGGTGA AAAAGCCACT TTGGAAACCC CAACATTTGC CCAGAAACGT CGGCGTACCC	1080
TGGATATGTT GATTAGATCT TTACACCAGG ATTTGATGCC AGATTGTCAT AAGAACATGC	1140
TTAATAGACG ATCTTTTAGT GATGTCTTAC CAGAGTCACC CAAGTCAGCG CGGAAGAAAG	1200
AGGAGGCCCG CCAGGCGGAG TTTGTTAGAA TAGGGCAGGC ACTAAACTG AAATCCATTG	1260
TGAGAGGGGA TGCTCCATCA AGCTTGGCAG CTTCAGGGAT CTGTAAAAAA GAGATGACCT	1320
TCCATCAGTG CCCGTGTTTG ACAGAACTCT GCCAGTGAAG CAAATGCATG TGCTTGAGAC	1380
CCTGGACCTT CTGGTTCTCA GAGCAGACAA AGGAAAAGAT GCTCGCCTCT TTGTCTTCAG	1440
GCTAAGTGCT CTGCAAAAGG GCCTTGAGGG GAAGCAGGCT GGGAAGAGCA GGTCTGACTG	1500
CAGAGAAAAC AAGTTGGAGA AAACAAAAGG CTGCCACCTG TATGCTATTA AACTCACCA	1560
CAGCAGAGAG CTGAGGATTG TGGTTGCAAT TCGGAATAAA CTGCTTCTGA TCACAAGAAA	1620
ACACAACAAG CCAAGCGGGG TCACCAGCAC CTCATTGTTA TCTCCCCTGT CTGAGTCACC	1680
TGTTGAAGAA TTCCAGTACA TCAGGGAGAT CTGTCTGTCT GACTCTCCCA TGGTGATGAC	1740

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CTTAGTGGAT GGGCCAGCTG AAGAGAGTGA CAATCTCATC TGTGTGGCTT ATCGACACCA 1800
ATTTGATGTG GTGAATGAGA GCACAGGAGA AGCCTTCAGG CTGCACCACG TGGAGGCCAA 1860
CAGGGTTAAT TTTGTTGCAG CTATTGATGT GTACGAAGAT GGAGAAGCTG GTTTGCTGTT 1920
GTGTTACAAC TACAGTTGCA TCTATAAAAA GGTTTGCCCC TTTAATGGTG GCTCTTTTTT 1980
GGTTCAACCT TCTGCGTCAG ATTTCCAGTT CTGTTGGAAC CAGGCTCCCT ATGCAATTGT 2040
CTGTGCTTTC CCGTATCTCC TGGCCTTCAC CACCGACTCC ATGGAGATCC GCCTGGTGGT 2100
GAACGGGAAC CTGGTCCACA CTGCAGTCGT GCCGCAGCTG CAGCTGGTGG CCTCCAGGTC 2160
GGATATATAC TTCACAGCAA CTGCAGCTGT GAATGAGGTC TCATCTGGAG GCAGCTCCAA 2220
GGGGGCCAGT GCCCGAAATT CTCCTCAGAC ACCCCCGGGC CGAGATACTC CAGTATTTCC 2280
TTCTTCCCTG GGGGAAGGTG AAATTCAATC AAAAAATCTG TACAAGATTC CACTTAGAAA 2340
CCTCGTGGGC AGAAGCATCG AACGACCTCT GAAGTCACCC TTAGTCTCCA AGGTCATCAC 2400
CCCACCCACT CCCATCAGTG TGGGCCTTGC TGCCATTCCA GTCACGCACT CCTTGTCCTT 2460
GTCTCGCATG GAGATCAAAG AAATAGCAAG CAGGACCCGC AGGGAACCTAC TGGGCCTCTC 2520
GGATGAAGGT GGACCCAAGT CAGAAGGAGC GCCAAAGGCC AAATCAAAAC CCCGGAAGCG 2580
GTTAGAAGAA AGCCAAGGAG GCCCCAAGCC AGGGGCAGTG AGGTCATCTA GCAGTGACAG 2640
GATCCCATCA GGCTCCTTGG AAAGTGCTTC TACTTCCGAA GCCAACCCTG AGGGGCACTC 2700
AGCCAGCTCT GACCAGGACC CTGTGGCAGA CAGAGAGGGC AGCCCGGTCT CCGGCAGCAG 2760
CCCCTTCCAG CTCACGGCTT TCTCCGATGA AGACATTATA GACTTGAAGT AACAGAGTTG 2820
AATCTCATTT GCCATCTTTA GTTTTCTTAT GGAGGTTTAT ACTCTTTAAA CAGTTCTGAT 2880
GTAATTTCTC AACAAAATGT GGCTTTTAGC CTGTCAGTGA TCTATTGGAC CAAACCTTCT 2940
GCACACTCGG CCAGTTCCCT CTCCAATGTC CGGTGCCATC TTTCTGACC TTTGTTTCTT 3000
TCTGTTTCAGG AACCATCAGT CCCCTTGTA TAAAGGTGGT AGATTTTCATT GAGGTTTTAG 3060
ATTGAAACTT TGAATAAATC AAAAATACTC ATTCTTAAAA AAAAAAAAAA AAAAAAAAAA 3119

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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Asn Leu Asp Lys Phe Glu Lys Gly Pro Arg Glu Ile Phe His Pro
1 5 10 15
Glu Ile Gln Lys Asp Leu Leu Val Leu Glu Glu Gln Glu Gly Ser Val
20 25 30
Asn Phe Lys Phe Gly Val Leu Phe Ala Lys Asp Gly Gln Leu Thr Asp
35 40 45
Asp Glu Met Phe Ser Asn Glu Ile Gly Ser Glu Pro Phe Gln Lys Phe
50 55 60
Leu Asn Leu Leu Gly Asp Thr Ile Thr Leu Lys Gly Trp Thr Gly Tyr
65 70 75 80
Arg Gly Gly Leu Asp Thr Lys Asn Asp Thr Thr Gly Ile His Ser Val
85 90 95
Tyr Thr Val Tyr Gln Gly His Glu Ile Met Phe His Val Ser Thr Met
100 105 110
Leu Pro Tyr Ser Lys Glu Asn Lys Gln Gln Val Glu Arg Lys Arg His
115 120 125
Ile Gly Asn Asp Ile Val Thr Ile Val Phe Gln Glu Gly Glu Glu Ser
130 135 140
Ser Pro Ala Phe Lys Pro Ser Met Ile Arg Ser His Phe Thr His Ile
145 150 155 160
Phe Ala Leu Val Arg Tyr Asn Gln Gln Asn Asp Asn Tyr Arg Leu Lys
165 170 175
Ile Phe Ser Glu Glu Ser Val Pro Leu Phe Gly Pro Pro Leu Pro Thr
180 185 190
Pro Pro Val Phe Thr Asp His Gln Glu Phe Arg Asp Phe Leu Leu Val
195 200 205
Lys Leu Ile Asn Gly Glu Lys Ala Thr Leu Glu Thr Pro Thr Phe Ala
210 215 220
Gln Lys Arg Arg Arg Thr Leu Asp Met Leu Ile Arg Ser Leu His Gln
225 230 235 240
Asp Leu Met Pro Asp Leu His Lys Asn Met Leu Asn Arg Arg Ser Phe
245 250 255
Ser Asp Val Leu Pro Glu Ser Pro Lys Ser Ala Arg Lys Lys Glu Glu
260 265 270
Ala Arg Gln Ala Glu Phe Val Arg Ile Gly Gln Ala Leu Lys Leu Lys
275 280 285
Ser Ile Val Arg Gly Asp Ala Pro Ser Ser Leu Ala Ala Ser Gly Ile
290 295 300

Cys Lys Lys Glu Met Thr Phe His Gln Cys Pro Cys Leu Thr Glu Leu
 305 310 315 320

Cys Gln

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GACTTTTATA AAAAAGTCAA GCAGTACAAA AGGGTGTAAG GTGAAGTTAC TGTCCTTCCC	60
CTCCATAAAC CCCCTGACCT TGGGAAACTG TTGTTAACAG TTACTTGGGT AACTTTTCAG	120
ATATTTTGTA TGCATGTACA AATGTGAGTA TCTAATGTAA AAAAATCAAA CCAAGATAAA	180
GTGTAAACTG CTATGATGGA ATCCTGCCTT GTTCTGCTAT TAGTCTTCTG TTTAATAATC	240
AGCTTTGGTA TTAGGACAGT GGTAGGAAGA AGCCAGTATG TCCTGCAACA TAATTTGTGG	300
TTCTGGACTG GTCAGGATTT CCTGAATGCA GCCTTTATCT GGAAGCTCTG CCCTTCTCCA	360
TCTGGGATAC GCTTTTTTCAT CCATCAAAAC TGTCATCTCC CTCTGTGAAG CCTTCCCTGA	420
CTATTCTCTG TCCCTCTTTC CTCTCTTCCC ACAAACACAA CTGTGTACGC GTGTCACCAA	480
AGAGTTAATC GTGCTTTTCT CTGTGCTACT TTTATACSTA GTATATGGTC CATTGTTTTG	540
CACTTAATAC ACTCTCTTGT AATGATTTGT TTACATGTCA GTCTCCCAGC CAGACTGAGA	600
GCTCACCAAG GGCAGAAGCC GTGTTTTGTT TACTGCTGTA TTCCTGGTAC CTGGTACAAT	660
GCTTGGCATA CAGTTGGATG AACGGGAAAG TAATCTGAGC TGCCGGTGCT GTGGCAGTGC	720
AAAGTGGGCA TATTTGTGCC CTTGGACCAG ATGTAGCCCT TGATGCATTT TGCAGGAACA	780
CGGCTTAGTT ATTGTTTACT TTGAAGCCCT TTTGCCTCTA CTCTCTCCCA TATATCTTCT	840
CCTGACAGGG TGAAGTCACC TATAGCATTT CCTAGTGTAT GGAAGTATTA ATTTCTTTCT	900
TTACTGGAAG AGCTACTAGC TTTTCTTCAT ACAGTTTCCT CTGCTCCAGT TTCATAAGTT	960
TCTTTTTTGGC TTGTATCTGT TTAGGATCAG GTGATATGGC TTCATTTCTC ATGACTGAAG	1020
CCCGGCAACA TAACACTGAA ATTCGAATGG CAGTCAGCAA AGTGGCTGAT AAAATGGATC	1080
ATCTCATGAC TAAGGTTGAA GAGTTACAGA AACATAGTGC TGGCAATTCC ATGCTTATTC	1140

CTAGCATGTC AGTTACAATG GAAACAAGCA TGATTATGAG CAACATCCAG CGAATCATTC 1200
 AGGCCAAGGT GACAGAGGAG TTAGCAGCGG CCACTGCACA GKTCTCTCAT CTGCAGCTGA 1260
 AAATGACTTG CTCACCAAAA AAAGGAAACA GAGCTGCAGA TGCAGCTGAC AGAAAGCCTG 1320
 AAGGAGACAG ATCTTCTCAG GGGCCAGCTC ACCAAAGTGC AGGCAAAGCT CTCAGAGCTC 1380
 CAAGAAACYT CTGAGCAAGC ACAGTCCAAA TTCAAAAGTG AAAAGCAGAA CCGGAAACAA 1440
 CTGGAActCA AGGTGACATC CCTGGAGGAG GAACTGACTG ACCTTCGAGT TGAGAAGGAG 1500
 TCCTTGAAA AGGTAAGCTC TACAACCCAG TTTGCCAGAA TTAGCTGTTT AATAAACATT 1560
 TTTATTTTCC TTTTACAAAA AAAAAAAAAA AA 1592

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Glu	Val	Leu	Ile	Ser	Phe	Phe	Thr	Gly	Arg	Ala	Thr	Ser	Phe	Ser	1	5	10	15
Ser	Tyr	Ser	Phe	Leu	Cys	Ser	Ser	Phe	Ile	Ser	Phe	Phe	Leu	Ala	Cys	20	25	30	
Ile	Cys	Leu	Gly	Ser	Gly	Asp	Met	Ala	Ser	Phe	Leu	Met	Thr	Glu	Ala	35	40	45	
Arg	Gln	His	Asn	Thr	Glu	Ile	Arg	Met	Ala	Val	Ser	Lys	Val	Ala	Asp	50	55	60	
Lys	Met	Asp	His	Leu	Met	Thr	Lys	Val	Glu	Glu	Leu	Gln	Lys	His	Ser	65	70	75	80
Ala	Gly	Asn	Ser	Met	Leu	Ile	Pro	Ser	Met	Ser	Val	Thr	Met	Glu	Thr	85	90	95	
Ser	Met	Ile	Met	Ser	Asn	Ile	Gln	Arg	Ile	Ile	Gln	Ala	Lys	Val	Thr	100	105	110	
Glu	Glu	Leu	Ala	Ala	Ala	Thr	Ala	Gln	Xaa	Ser	His	Leu	Gln	Leu	Lys	115	120	125	
Met	Thr	Cys	Ser	Pro	Lys	Lys	Gly	Asn	Arg	Ala	Ala	Asp	Ala	Ala	Asp	130	135	140	
Arg	Lys	Pro	Glu	Gly	Asp	Arg	Ser	Ser	Gln	Gly	Pro	Ala	His	Gln	Ser	145	150	155	160

Ala Gly Lys Ala Leu Arg Ala Pro Arg Asn Xaa
 165 170

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1694 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

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GGGAAACGGG AAGCCGCTGC AAGTCCACCG CCTCAGCTAC CCAGATTGGG ATCTGCCCAG      60
GCCCCGCTTTA TGGACTAGTG TGGGCGGCAG GCTCCTTTCC GTCCCTGCCC TGCTGTACCC      120
CGCTCCTTGG AGACCCCTTG TATCCCTCCC GCAAGGTGGA ATCCGCAGGC TGGAGGCTCC      180
CAGGGGAGGC AAACGCCTGG CCCTGCCCTG CCCCACGCCG CACCATGACC CTCCTGCTGC      240
TGCCCCCTTCT GCTGGCCTCT CTGCTCGCGT CCTGCTCCTG TAACAAAGCC AACAAGCACA      300
AGCCATGGAT TGAGGCAGAG TACCAGGGCA TCGTCATGGA GAATGACAAC ACGGTCCTAC      360
TGAATCCACC ACTCTTTGCC TTGGACAAGG ATGCCCCGCT GCGCTATGCA GGTGAGATCT      420
GCGGCTTCCG GCTCCATGGG TCTGGGGTGC CCTTTGAGGC TGTGATCCTT GACAAGGCGA      480
CAGGAGAGGG GCTGATCCGG GCCAAGGAGC CTGTGGACTG CGAGGCCCAG AAGGAACACA      540
CCTTCACCAT CCAGGCCTAT GACTGTGGCG AGGGCCCCGA CGGGGCCAAC ACCAAGAAGT      600
CCCACAAGGC CACTGTGCAT GTGCGGGTCA ACGATGTGAA CGAGTTTGCC CCAGTGTTTG      660
TGGAACGGCT GTATCGTGCG GCTGTGACAG AGGGGAAGCT GTACGATCGC ATCCTGCGGG      720
TGGAAGCCAT TGACGGTGAC TGCTCCCCCC AGTACAGCCA GATCTGCTAC TATGAGATTC      780
TCACACCCAA CACCCCTTTC CTCATTGACA ATGACGGGAA CATTGAGAAC ACAGAGAAGC      840
TGCAGTACAG TGGTGAGAGG CTCTATAAGT TTACAGTGAC AGCTTATGAC TGTGGGAAGA      900
AGCGGGCAGC AGATGATGCT GAGGTGGAGA TTCAGGTGAA GCCCACCTGT AAACCCAGCT      960
GGCAAGGCTG GAACAAAAGG ATCGAATATG CACCAGGTGC TGGGAGCTTG GCTTTGTTCC     1020
CTGGTATCCG CCTGGAGACC TGTGATGAAC CACTCTGGAA CATTGAGGCC ACCATAGAGC     1080
TGCAGACCAG CCATGTGGCC AAGGGCTGTG ACCGTGACAA CTACTCAGAG CGGGCGCTGC     1140
GGAAACTCTG TGGTGCTGCC ACTGGGGAGG TGGATCTGTT GCCCATGCCT GGCCCCAATG     1200
CCAACTGGAC AGCAGGACTC TCGGTGCACT ACAGCCAGGA CAGCAGCCTG ATCTACTGGT     1260

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TCAATGGCAC CCAGGCTGTG CAGGTGCCCC TGGGTGGCCC CAGTGGGCTG GGCTCTGGGC 1320
 CCCAGGACAG CCTCAGTGAC CACTTCACCC TGTCTTCTG GATGAAGCAT GGCGTAACTC 1380
 CCAACAAGGG CAAGAAGGAA GAGGAAACCA TCGTATGTAA CACTGTCCAG AATGGTGAGC 1440
 CTCCCCTCCA GGCCTAGCC AGAGGGGGAA ACTGGCTTCT TGTCCCGCCT CTGTCACTGC 1500
 CCAGTGTGTG ACTGTGAACA GGTCACCTCC CCTCTCTTCA TTTGTGAGGT GCAAGTGCCA 1560
 GGTGTGATAT GCCTTGATTC TGTGCTTTAT CCCCAACATG ACATGTTGGA TCGTAAAAAA 1620
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1680
 AAAAAAAAAA AAAA 1694

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Thr	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Ala	Ser	Leu	Leu	Ala	Ser	1	5	10	15
Cys	Ser	Cys	Asn	Lys	Ala	Asn	Lys	His	Lys	Pro	Trp	Ile	Glu	Ala	Glu	20	25	30	
Tyr	Gln	Gly	Ile	Val	Met	Glu	Asn	Asp	Asn	Thr	Val	Leu	Leu	Asn	Pro	35	40	45	
Pro	Leu	Phe	Ala	Leu	Asp	Lys	Asp	Ala	Pro	Leu	Arg	Tyr	Ala	Gly	Glu	50	55	60	
Ile	Cys	Gly	Phe	Arg	Leu	His	Gly	Ser	Gly	Val	Pro	Phe	Glu	Ala	Val	65	70	75	80
Ile	Leu	Asp	Lys	Ala	Thr	Gly	Glu	Gly	Leu	Ile	Arg	Ala	Lys	Glu	Pro	85	90	95	
Val	Asp	Cys	Glu	Ala	Gln	Lys	Glu	His	Thr	Phe	Thr	Ile	Gln	Ala	Tyr	100	105	110	
Asp	Cys	Gly	Glu	Gly	Pro	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Ser	His	Lys	115	120	125	
Ala	Thr	Val	His	Val	Arg	Val	Asn	Asp	Val	Asn	Glu	Phe	Ala	Pro	Val	130	135	140	
Phe	Val	Glu	Arg	Leu	Tyr	Arg	Ala	Ala	Val	Thr	Glu	Gly	Lys	Leu	Tyr				

145		150		155		160
Asp Arg Ile Leu Arg Val Glu Ala Ile Asp Gly Asp Cys Ser Pro Gln						
	165			170		175
Tyr Ser Gln Ile Cys Tyr Tyr Glu Ile Leu Thr Pro Asn Thr Pro Phe						
	180			185		190
Leu Ile Asp Asn Asp Gly Asn Ile Glu Asn Thr Glu Lys Leu Gln Tyr						
	195		200		205	
Ser Gly Glu Arg Leu Tyr Lys Phe Thr Val Thr Ala Tyr Asp Cys Gly						
	210		215		220	
Lys Lys Arg Ala Ala Asp Asp Ala Glu Val Glu Ile Gln Val Lys Pro						
	225		230		235	240
Thr Cys Lys Pro Ser Trp Gln Gly Trp Asn Lys Arg Ile Glu Tyr Ala						
		245		250		255
Pro Gly Ala Gly Ser Leu Ala Leu Phe Pro Gly Ile Arg Leu Glu Thr						
		260		265		270
Cys Asp Glu Pro Leu Trp Asn Ile Gln Ala Thr Ile Glu Leu Gln Thr						
	275		280		285	
Ser His Val Ala Lys Gly Cys Asp Arg Asp Asn Tyr Ser Glu Arg Ala						
	290		295		300	
Leu Arg Lys Leu Cys Gly Ala Ala Thr Gly Glu Val Asp Leu Leu Pro						
	305		310		315	320
Met Pro Gly Pro Asn Ala Asn Trp Thr Ala Gly Leu Ser Val His Tyr						
		325		330		335
Ser Gln Asp Ser Ser Leu Ile Tyr Trp Phe Asn Gly Thr Gln Ala Val						
	340		345		350	
Gln Val Pro Leu Gly Gly Pro Ser Gly Leu Gly Ser Gly Pro Gln Asp						
	355		360		365	
Ser Leu Ser Asp His Phe Thr Leu Ser Phe Trp Met Lys His Gly Val						
	370		375		380	
Thr Pro Asn Lys Gly Lys Lys Glu Glu Glu Thr Ile Val Cys Asn Thr						
	385		390		395	400
Val Gln Asn Gly Glu Pro Pro Leu Gln Ala Leu Ala Arg Gly Gly Asn						
		405		410		415
Trp Leu Leu Val Pro Pro Leu Ser Leu Pro Ser Val						
	420		425			

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1309 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGGTCCTCC TTTGCAGAGG TGGTGCGGAG CTCCTGTTTG ACGGTATTAA GAAACATCGA	60
GTCACCTTTGC CTGGACAGGA GGAACCCTGG GACATCCGGA ACCTGCTCAT CTGGATCAAG	120
AAGAATTTGC TAAAAGAGCG GCCAGAGTTG TTCATCCAGG GAGACAGCGT GCGGCCAGGA	180
ATTCTGGTGC TGATTAACGA TGCCGACTGG GAGCTACTGG GTGAGCTGGA CTACCAGCTT	240
CAGGACCAGG ACAGCGTCCT CTTTCATCTCC ACTCTGCACG GCGGCTGAGG GCCCTTCTCT	300
GGGCCTGGGC ACCCTTAGAG GGGAGAACGA AGCAATCAGA CATCCCCTTG GGCCCTGCTT	360
CCAGGTCTCC CTGTCCCCCT TGCCTGCCTT CTTCCCTGCT CTGTCCCCTA AGCTCCCTCC	420
AGGCAGGGAA AAGAGGCCAG GTGCTAAAAA TGAGCCTTTC TCAAGCACGT GAGCAGCGGA	480
AGGCAGACAG GCGCCAGAGC CCAGCACTCC CTTTTCCAGC AGCTGTGGTG GGGGAGGGTT	540
CCCCTCCAGT TTGTCAAGAG TTGAAGGAGG CTCTGTGGCC AGGTGACCTG GCTGCCTTCC	600
ACTCCTTGTA CCTCAGTCTA AACATGGAGT GGCCGCTGAC AAGGCGCTCC AGCCCCAGAG	660
CCAGCGTCTT CATGGGGAAG ATGAATGGAC CTGAGTAGCT GAAGGAAGGC CCCTCCCTAC	720
CCAAAGACTG GAGGCTTCTC AGCCTCAATT TCCCTGTCTG TACAGCTGAG GGCTCTGCCT	780
GTCCCCCACT GCTATCAGTA TGGAACCCCA GCTGGGGTCC CCTATTGAGT GCCGACTCCC	840
CCCACCGCCA GCAGCTGCTC CTCCAGCCAC ACCCTTCCTG CTCCCCCCAC CCYTAGCCCT	900
TGACCCTGGC TGGCCTGCCC CGCTCCACAG GCCACCAGAT GGGCTCCTGA GACCCTCCCC	960
AGGCTGCTTA CAGCTCATTC TGCTGGGGGT AGAGATGAGG GGAGGGAGTA AGTTAAACCT	1020
TGGACTAGCA AGTAGAAGCC TGGGGGGATG CGTGTGCCTC AGTTTCCTCC TCCACAACCTG	1080
AATATAGTGG CTGAAAACCTG GGGAGATACT TGATGGCGCG AATGTCCGTT TTCTCTCCCT	1140
TCCCACCTCC TGCAGGAAGC AGGACGGGGC AGGCAGCACC TGGTAGGCAC AGTGCTTTGC	1200
CCCTCCTCCC CTTCCCTTCT GGAAGTCTTG GGGCCTCAGT GCTTGCAACA GCCGGCCTTG	1260
GGCAAATAAA AGACTAGGTT GTTTACTAAA AAAAAAAAAA AAAAAAAAAA	1309

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
Met Ala Arg Met Ser Val Phe Ser Pro Phe Pro Pro Pro Ala Gly Ser
1           5           10          15

Arg Thr Gly Gln Ala Ala Pro Gly Arg His Ser Ala Leu Pro Leu Leu
20          25          30

Pro Phe Pro Ser Gly Ser Leu Gly Ala Ser Val Leu Ala Thr Ala Gly
35          40          45

Leu Gly Gln Ile Lys Asp
50
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
GGCCCGTGCG CTCCATCAAC CACGCCAGCC TCATCTCTGC ACTCTCCCGG GACTATCGCA      60
ACCTGAAGCC CAGTGCTGTT GCCCCACAGA GAAAGATGCC ACTGGATGAC ACCAAACTGA      120
TTATCCACCA GACACTCAGC GTCTTAGAAG ATATTGTGGA GAATATCTCG GGGGAGTCCA      180
CCAAGTCTCG ACAGATTTGC TACCAGTCGC TGCAGGAATC TGTTCAGGTC TCCCTGGCCC      240
TCTTTCCAGC TTTTATCCAT CAGTCAGATG TGA CTGATGA GATGCTGAGC TTCTTCCTCA      300
CTCTGTTTCG AGGCCTTAGA GTACAGATGG GTGTGCCTTT CACTGAGCAA ATCATACAGA      360
CTTTCCTCAA CATGTTTACC AGAGAGCAGT TAGCCGAGAG CATCCTCCAC GAGGGCAGCA      420
CAGGCTGCCG GGTGGTGGAG AAGTTTCTGA AGATCCTGCA GGTGGTGGTC CAGGAGCCAG      480
GCCAGGTGTT CAAGCCCTTC CTCCCCAGCA TCATCGCCCT GTGCATGGAG CAAGTGTATC      540
CCATCATTGC CGAGCGTCCC TCCCCTGATG TGAAGGCCGA GCTGTTTGAG CTCCTTTTCC      600
GGACGCTCCA TCACAACTGG AGGTACTTCT TCAAGTCCAC CGTGCTGGCC AGTGTCAGCA      660
GGGGGATCGC TGAGGAGCAG ATGGAGAATG AGCCCCAGTT CAGTGCCATC ATGCAGGCTT      720
TCGGACAGTC CTTTCTCCAG CCCGACATCC ACCTTTTTTAA ACAAATCTC TTCTACTTGG      780
```

```

AGACTCTCAA CACCAAGCAG AAGCTGTACC ACAAGAAGAT CTTCCGGACT GCCATGCTGT      840
TCCAGTTTGT GAACGTGCTG CTCCAGGTCC TGGTCCACAA GTCCCATGAT CTTCTGCAGG      900
AGGAGATTGG CATCGCCATC TACAACATGG CCTCAGTCGA CTTTGATGGC TTCTTTGCCG      960
CCTTCCTCCC AGAGTTCTTG ACCAGCTGTG ATGGTGTGGA TGCCAACCAG AAAAGTGTGC     1020
TGGGGCGGAA TTTCAAGATG GATCGGGACC TGCCCTCATT CACCCAGAAT GTGCACAGGC     1080
TGGTCAACGA CCTGCGCTAC TACAGACTCT GCAACGACAG CCTGCCCCCT GGCAGTGTGA     1140
AGCTCTAGGC CTGCTACTGC CTGGGGACAC GGACTTCTGC TGCTGCCACC TGCGCCAGCC     1200
CTACCTTCCA CCACAGATGT CTCCCAGATG GGCCTTGGTC ACACTCCTTG GCTTCTCCCA     1260
CCGCAAGCAA CGCTGCCTGC CTCTGCCGCT CCTCCACATC TTGCCGCTGC CCAGCAGAGC     1320
TGGCTTCTGG GTCCACCTGA GCACTGGACG GTGCTCCAG GCGTTGGAG CAGGCGGAGG     1380
GGTGTGTGGC CAGGTACTAG GAGGCACCAG GAAATCCCGC GGGGTGGCCC ATGCAGACCA     1440
GGCGCACGTG GTCATGGGG CAGAATTGCC AAGGACAGCT CACGACAGTG CMACCTTCTC     1500
ACCATTCCAG CCAAGGAGAG ATGTGACGTT GGAAMTGYTY TGGCAMTTYT GTCAAGCCTC     1560
CCCCGCCCCA ATGCCTTGA RATYTYTGCT CTTTGTGAGA GATTTGCAA GACTCAMGTT     1620
TTTGTGTGTT TCTCATCATT CCATTGTGAT ACTAAGAAAC TAAGAAGCTT AATGAAAAGA     1680
AATAAAATGC CTATGTTGTT GTTCTAGGRR AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA     1740

```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Met  Pro  Leu  Asp  Asp  Thr  Lys  Leu  Ile  Ile  His  Gln  Thr  Leu  Ser  Val
1              5              10              15

Leu  Glu  Asp  Ile  Val  Glu  Asn  Ile  Ser  Gly  Glu  Ser  Thr  Lys  Ser  Arg
                20              25              30

Gln  Ile  Cys  Tyr  Gln  Ser  Leu  Gln  Glu  Ser  Val  Gln  Val  Ser  Leu  Ala
                35              40              45

Leu  Phe  Pro  Ala  Phe  Ile  His  Gln  Ser  Asp  Val  Thr  Asp  Glu  Met  Leu
50              55              60

```


Ser	Phe	Phe	Leu	Thr	Leu	Phe	Arg	Gly	Leu	Arg	Val	Gln	Met	Gly	Val	65	70	75	80
Pro	Phe	Thr	Glu	Gln	Ile	Ile	Gln	Thr	Phe	Leu	Asn	Met	Phe	Thr	Arg	85	90	95	
Glu	Gln	Leu	Ala	Glu	Ser	Ile	Leu	His	Glu	Gly	Ser	Thr	Gly	Cys	Arg	100	105	110	
Val	Val	Glu	Lys	Phe	Leu	Lys	Ile	Leu	Gln	Val	Val	Val	Gln	Glu	Pro	115	120	125	
Gly	Gln	Val	Phe	Lys	Pro	Phe	Leu	Pro	Ser	Ile	Ile	Ala	Leu	Cys	Met	130	135	140	
Glu	Gln	Val	Tyr	Pro	Ile	Ile	Ala	Glu	Arg	Pro	Ser	Pro	Asp	Val	Lys	145	150	155	160
Ala	Glu	Leu	Phe	Glu	Leu	Leu	Phe	Arg	Thr	Leu	His	His	Asn	Trp	Arg	165	170	175	
Tyr	Phe	Phe	Lys	Ser	Thr	Val	Leu	Ala	Ser	Val	Gln	Arg	Gly	Ile	Ala	180	185	190	
Glu	Glu	Gln	Met	Glu	Asn	Glu	Pro	Gln	Phe	Ser	Ala	Ile	Met	Gln	Ala	195	200	205	
Phe	Gly	Gln	Ser	Phe	Leu	Gln	Pro	Asp	Ile	His	Leu	Phe	Lys	Gln	Asn	210	215	220	
Leu	Phe	Tyr	Leu	Glu	Thr	Leu	Asn	Thr	Lys	Gln	Lys	Leu	Tyr	His	Lys	225	230	235	240
Lys	Ile	Phe	Arg	Thr	Ala	Met	Leu	Phe	Gln	Phe	Val	Asn	Val	Leu	Leu	245	250	255	
Gln	Val	Leu	Val	His	Lys	Ser	His	Asp	Leu	Leu	Gln	Glu	Glu	Ile	Gly	260	265	270	
Ile	Ala	Ile	Tyr	Asn	Met	Ala	Ser	Val	Asp	Phe	Asp	Gly	Phe	Phe	Ala	275	280	285	
Ala	Phe	Leu	Pro	Glu	Phe	Leu	Thr	Ser	Cys	Asp	Gly	Val	Asp	Ala	Asn	290	295	300	
Gln	Lys	Ser	Val	Leu	Gly	Arg	Asn	Phe	Lys	Met	Asp	Arg	Asp	Leu	Pro	305	310	315	320
Ser	Phe	Thr	Gln	Asn	Val	His	Arg	Leu	Val	Asn	Asp	Leu	Arg	Tyr	Tyr	325	330	335	
Arg	Leu	Cys	Asn	Asp	Ser	Leu	Pro	Pro	Gly	Thr	Val	Lys	Leu	340	345	350			

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ANTGTCTTGA CTACAAGCTC CACGGGGGC

29

- (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TNGCCAAGGA GAAAGCGAGG CAGACAAGG

29

- (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ANATCGACTC TTTGCATCGC ACATTTTGT

29

- (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CNTTCTTCGG ACTTATGTTT GAATCTATC

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CNTTCCTCTT AGATCTCAGT ATCCACCTC

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CNCAGACAGG GGAGATAACA ATGAGGTGC

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TNCTATAGGT GACTTCACCC TGTCAGGAG

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TNTTACAGGA GCAGGACGCG AGCAGAGAG

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ANTCAGTTGT GGAGGAGGAA ACTGAGGCA

29

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CNTCGAAACA GAGTGAGGAA GAAGCTCAG

29

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Val	Ala	Trp	Arg	Ser	Ala	Phe	Leu	Val	Cys	Leu	Ala	Phe	Ser	Leu	
1				5				10						15		
Ala	Thr	Leu	Val	Gln	Arg	Gly	Ser	Gly	Asp	Phe	Asp	Asp	Phe	Asn	Leu	
			20					25					30			
Glu	Asp	Ala	Val	Lys	Glu	Thr	Ser	Ser	Val	Lys	Gln	Pro	Trp	Asp	His	
		35					40					45				
Thr	Thr	Thr	Thr	Thr	Thr	Asn	Arg	Pro	Gly	Thr	Thr	Arg	Ala	Pro	Ala	
		50				55					60					
Lys	Pro	Pro	Gly	Ser	Gly	Leu	Asp	Leu	Ala	Asp	Ala	Leu	Asp	Asp	Gln	
65				70					75						80	
Asp	Asp	Gly	Arg	Arg	Lys	Pro	Gly	Ile	Gly	Gly	Arg	Glu	Arg	Trp	Asn	
			85					90						95		
His	Val	Thr	Thr	Thr	Thr	Lys	Arg	Pro	Val	Thr	Thr	Arg	Ala	Pro	Ala	
			100					105					110			
Asn	Thr	Leu	Gly	Asn	Asp	Phe	Asp	Leu	Ala	Asp	Ala	Leu	Asp	Asp	Arg	
		115					120					125				
Asn	Asp	Arg	Asp	Asp	Gly	Arg	Arg	Lys	Pro	Ile	Ala	Gly	Gly	Gly	Gly	
		130				135					140					
Phe	Ser	Asp	Lys	Asp	Leu	Glu	Asp	Ile	Val	Gly	Gly	Gly	Glu	Tyr	Lys	
145					150					155					160	
Pro	Asp	Lys	Gly	Lys	Gly	Asp	Gly	Arg	Tyr	Gly	Ser	Asn	Asp	Asp	Pro	
			165					170						175		
Gly	Ser	Gly	Met	Val	Ala	Glu	Pro	Gly	Thr	Ile	Ala	Gly	Val	Ala	Ser	
			180					185					190			
Ala	Leu	Ala	Met	Ala	Leu	Ile	Gly	Ala	Val	Ser	Ser	Tyr	Ile	Ser	Tyr	
		195					200					205				
Gln	Gln	Lys	Lys	Phe	Cys	Phe	Ser	Ile	Gln	Gln	Gly	Leu	Asn	Ala	Asp	
		210					215				220					

Tyr Val Lys Gly Glu Asn Leu Glu Ala Val Val Cys Glu Glu Pro Gln
 225 230 235 240

Val Lys Tyr Ser Thr Leu His Thr Gln Ser Ala Glu Pro Pro Pro Pro
 245 250 255

Pro Glu Pro Ala Arg Ile
 260

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met His Val Leu Glu Thr Leu Asp Leu Leu Val Leu Arg Ala Asp Lys
 1 5 10 15

Gly Lys Asp Ala Arg Leu Phe Val Phe Arg Leu Ser Ala Leu Gln Lys
 20 25 30

Gly Leu Glu Gly Lys Gln Ala Gly Lys Ser Arg Ser Asp Cys Arg Glu
 35 40 45

Asn Lys Leu Glu Lys Thr Lys Gly Cys His Leu Tyr Ala Ile Asn Thr
 50 55 60

His His Ser Arg Glu Leu Arg Ile Val Val Ala Ile Arg Asn Lys Leu
 65 70 75 80

Leu Leu Ile Thr Arg Lys His Asn Lys Pro Ser Gly Val Thr Ser Thr
 85 90 95

Ser Leu Leu Ser Pro Leu Ser Glu Ser Pro Val Glu Glu Phe Gln Tyr
 100 105 110

Ile Arg Glu Ile Cys Leu Ser Asp Ser Pro Met Val Met Thr Leu Val
 115 120 125

Asp Gly Pro Ala Glu Glu Ser Asp Asn Leu Ile Cys Val Ala Tyr Arg
 130 135 140

His Gln Phe Asp Val Val Asn Glu Ser Thr Gly Glu Ala Phe Arg Leu
 145 150 155 160

His His Val Glu Ala Asn Arg Val Asn Phe Val Ala Ala Ile Asp Val
 165 170 175

Tyr Glu Asp Gly Glu Ala Gly Leu Leu Leu Cys Tyr Asn Tyr Ser Cys
 180 185 190

Ile	Tyr	Lys	Lys	Val	Cys	Pro	Phe	Asn	Gly	Gly	Ser	Phe	Leu	Val	Gln				
		195						200				205							
Pro	Ser	Ala	Ser	Asp	Phe	Gln	Phe	Cys	Trp	Asn	Gln	Ala	Pro	Tyr	Ala				
		210				215					220								
Ile	Val	Cys	Ala	Phe	Pro	Tyr	Leu	Leu	Ala	Phe	Thr	Thr	Asp	Ser	Met				
225					230					235					240				
Glu	Ile	Arg	Leu	Val	Val	Asn	Gly	Asn	Leu	Val	His	Thr	Ala	Val	Val				
				245				250						255					
Pro	Gln	Leu	Gln	Leu	Val	Ala	Ser	Arg	Ser	Asp	Ile	Tyr	Phe	Thr	Ala				
			260					265					270						
Thr	Ala	Ala	Val	Asn	Glu	Val	Ser	Ser	Gly	Gly	Ser	Ser	Lys	Gly	Ala				
		275				280						285							
Ser	Ala	Arg	Asn	Ser	Pro	Gln	Thr	Pro	Pro	Gly	Arg	Asp	Thr	Pro	Val				
		290				295					300								
Phe	Pro	Ser	Ser	Leu	Gly	Glu	Gly	Glu	Ile	Gln	Ser	Lys	Asn	Leu	Tyr				
305				310						315				320					
Lys	Ile	Pro	Leu	Arg	Asn	Leu	Val	Gly	Arg	Ser	Ile	Glu	Arg	Pro	Leu				
			325					330						335					
Lys	Ser	Pro	Leu	Val	Ser	Lys	Val	Ile	Thr	Pro	Pro	Thr	Pro	Ile	Ser				
			340					345						350					
Val	Gly	Leu	Ala	Ala	Ile	Pro	Val	Thr	His	Ser	Leu	Ser	Leu	Ser	Arg				
		355				360						365							
Met	Glu	Ile	Lys	Glu	Ile	Ala	Ser	Arg	Thr	Arg	Arg	Glu	Leu	Leu	Gly				
	370					375					380								
Leu	Ser	Asp	Glu	Gly	Gly	Pro	Lys	Ser	Glu	Gly	Ala	Pro	Lys	Ala	Lys				
385				390						395				400					
Ser	Lys	Pro	Arg	Lys	Arg	Leu	Glu	Glu	Ser	Gln	Gly	Gly	Pro	Lys	Pro				
			405					410						415					
Gly	Ala	Val	Arg	Ser	Ser	Ser	Ser	Asp	Arg	Ile	Pro	Ser	Gly	Ser	Leu				
			420					425					430						
Glu	Ser	Ala	Ser	Thr	Ser	Glu	Ala	Asn	Pro	Glu	Gly	His	Ser	Ala	Ser				
		435				440						445							
Ser	Asp	Gln	Asp	Pro	Val	Ala	Asp	Arg	Glu	Gly	Ser	Pro	Val	Ser	Gly				
	450					455					460								
Ser	Ser	Pro	Phe	Gln	Leu	Thr	Ala	Phe	Ser	Asp	Glu	Asp	Ile	Ile	Asp				
465				470						475				480					
Leu	Lys																		

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTCTACTGAT ACGACACAAG ATCGGGAGAT TTTTGATCAC CATACTGAAG AGGATATAGA 60
TAAAAGTGCT AACAGTGTAT TGATAAAAAA CCTGAGCAGG ACCCATCTA GTTGACGAG 120
CTCTCTGGAT TCAATCAAGG CTGATGGGAC CTCTCTGGAC TTCAGCACTT ACCGCAGTAG 180
TCAAATGGAA TCACAGTTTC TCAGAGATAC TATTTGTGAA GAGAGCTTGA GGGAGAACT 240
CCAAGATGGG AGAATAACAA TAAGGGAGTT CTTTATACTT CTCCAGGTCC ACATCTTGAT 300
ACAGAAACCC CGACAGAGCA ATCTCCAGG CAATTTTACT GTAAACACAC CACCTACTCC 360
AGAAGACCTG ATGTTAAGTC AATATGTTTA CCGACCCAAG ATACAGATTT ATAGAGAAGA 420
TTGTGAGGCT CGTCGCCAAA AGATTGAAGA ATTAAAGCTT TCTGCATCGA ACCAAGATAA 480
GCTGTTGGTT GATATAAATA AGAACCTGTG GGAAAAAATG AGACACTGCT CTGACAAAGA 540
GCTGAAGGCC TTTGGAATTT ATCTTAACAA AATAAAGTCA TGTTTTACCA AGATGACTAA 600
AGTCTTCACT CACCAAGGAA AAGTGGCTCT GTATGGCAAG CTGGTGCAGT CAGCTCAGAA 660
TGAGAGGGAG AAACCTCAAA TAAAGATAGA TGAGATGGAT AAAATACTTA AGAAGATCGA 720
TAACTGCCTC ACTGAGATGG AAACAGAAAC TAAGAATTTG GAGGATGAAG AGAAAAACAA 780
TCCTGTGGAA GAATGGGATT CTGAAATGAG AGCTGCAGAA AAAGAATTGG AACAGCTGAA 840
AACTGAAGAG GAGGAGCTTC AAAGAAATCT CTTAGAACTG GAGGTACCAA AAGAGCAGAC 900
CCTTGCTCAA ATAGACTTTA TGCAAAAACA AAGAAATAGA ACTGAAGAGC TACTGGATCA 960
GTTGAGCTTG TCTGAGTGGG ATGTCGTTGA GTGGAGTGAT GATCAAGCTG TATTCACCTT 1020
TGTTTATGAC ACGATACAAC TCACCATCAC CTTTGAAGAG TCAGTTGTTG GTTTCCTTTT 1080
CCTGGACAAG CGTTATAGGA AGATTGTTGA TGTCAATTTT CAATCTCTGT TAGATGAGGA 1140
TCAAGCTCCT CCTTCCTCCC TTTTAGTTCA TAAGCTTATT TTCCAGTACG TTGAAGAAAA 1200
GGAATCCTGG AAGAAGACAT GTACAACCCA GCATCAGTTA CCCAAGATGC TTGAAGAATT 1260
CTCACTGGTA GTGCACCATT GCAGACTCCT TGGAGAGGAG ATTGAGTATT TAAAGAGATG 1320

GGGACCAAAT TATAACCTAA TGAACATAGA TATTAATAAT AATGAATTGA GACTTTTATT 1380
 CTCTAGCTCC GCAGCATTTG CAAAGTTTGA AATAACTTTG TTTCTCTCAG CCTATTATCC 1440
 ATCTGTACCA TTACCTTCCA CCATTTCAGAA TCACGTTGGG AACACTAGCC AAGATGATAT 1500
 TGCTACCATT CTATCTAAAG TGCCACTGGA GAACAACCTAC CTGAAGAATG TAGTCAAGCA 1560
 AATTTACCAA GATCTGTTTC AGGACTGCCA TTTCTACCAC TAGACCCTTG GACCACCATT 1620
 GGAACAACCA AGCAGAATGT ACTTGATATT ATTTTCAGGGT CCCATTGCTG TTCAGCCTTT 1680
 GTTTTTACGT CATTACAAGC TGAGTAAAAT TCCTTCTGAT GATGTTATAA AAAAAAAAAA 1740
 AAAAAAAAAA 1748

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Glu	Ser	Gln	Phe	Leu	Arg	Asp	Thr	Ile	Cys	Glu	Glu	Ser	Leu	Arg	1	5	10	15
Glu	Lys	Leu	Gln	Asp	Gly	Arg	Ile	Thr	Ile	Arg	Glu	Phe	Phe	Ile	Leu	20	25	30	
Leu	Gln	Val	His	Ile	Leu	Ile	Gln	Lys	Pro	Arg	Gln	Ser	Asn	Leu	Pro	35	40	45	
Gly	Asn	Phe	Thr	Val	Asn	Thr	Pro	Pro	Thr	Pro	Glu	Asp	Leu	Met	Leu	50	55	60	
Ser	Gln	Tyr	Val	Tyr	Arg	Pro	Lys	Ile	Gln	Ile	Tyr	Arg	Glu	Asp	Cys	65	70	75	80
Glu	Ala	Arg	Arg	Gln	Lys	Ile	Glu	Glu	Leu	Lys	Leu	Ser	Ala	Ser	Asn	85	90	95	
Gln	Asp	Lys	Leu	Leu	Val	Asp	Ile	Asn	Lys	Asn	Leu	Trp	Glu	Lys	Met	100	105	110	
Arg	His	Cys	Ser	Asp	Lys	Glu	Leu	Lys	Ala	Phe	Gly	Ile	Tyr	Leu	Asn	115	120	125	
Lys	Ile	Lys	Ser	Cys	Phe	Thr	Lys	Met	Thr	Lys	Val	Phe	Thr	His	Gln	130	135	140	
Gly	Lys	Val	Ala	Leu	Tyr	Gly	Lys	Leu	Val	Gln	Ser	Ala	Gln	Asn	Glu	145	150	155	160

Arg	Glu	Lys	Leu	Gln	Ile	Lys	Ile	Asp	Glu	Met	Asp	Lys	Ile	Leu	Lys	
				165					170					175		
Lys	Ile	Asp	Asn	Cys	Leu	Thr	Glu	Met	Glu	Thr	Glu	Thr	Lys	Asn	Leu	
			180					185					190			
Glu	Asp	Glu	Glu	Lys	Asn	Asn	Pro	Val	Glu	Glu	Trp	Asp	Ser	Glu	Met	
		195					200					205				
Arg	Ala	Ala	Glu	Lys	Glu	Leu	Glu	Gln	Leu	Lys	Thr	Glu	Glu	Glu	Glu	
	210					215					220					
Leu	Gln	Arg	Asn	Leu	Leu	Glu	Leu	Glu	Val	Pro	Lys	Glu	Gln	Thr	Leu	
225				230						235					240	
Ala	Gln	Ile	Asp	Phe	Met	Gln	Lys	Gln	Arg	Asn	Arg	Thr	Glu	Glu	Leu	
			245						250						255	
Leu	Asp	Gln	Leu	Ser	Leu	Ser	Glu	Trp	Asp	Val	Val	Glu	Trp	Ser	Asp	
			260					265					270			
Asp	Gln	Ala	Val	Phe	Thr	Phe	Val	Tyr	Asp	Thr	Ile	Gln	Leu	Thr	Ile	
		275					280					285				
Thr	Phe	Glu	Glu	Ser	Val	Val	Gly	Phe	Pro	Phe	Leu	Asp	Lys	Arg	Tyr	
	290					295					300					
Arg	Lys	Ile	Val	Asp	Val	Asn	Phe	Gln	Ser	Leu	Leu	Asp	Glu	Asp	Gln	
305					310					315					320	
Ala	Pro	Pro	Ser	Ser	Leu	Leu	Val	His	Lys	Leu	Ile	Phe	Gln	Tyr	Val	
			325						330					335		
Glu	Glu	Lys	Glu	Ser	Trp	Lys	Lys	Thr	Cys	Thr	Thr	Gln	His	Gln	Leu	
			340					345					350			
Pro	Lys	Met	Leu	Glu	Glu	Phe	Ser	Leu	Val	Val	His	His	Cys	Arg	Leu	
		355					360					365				
Leu	Gly	Glu	Glu	Ile	Glu	Tyr	Leu	Lys	Arg	Trp	Gly	Pro	Asn	Tyr	Asn	
	370					375					380					
Leu	Met	Asn	Ile	Asp	Ile	Asn	Asn	Asn	Glu	Leu	Arg	Leu	Leu	Phe	Ser	
385					390					395					400	
Ser	Ser	Ala	Ala	Phe	Ala	Lys	Phe	Glu	Ile	Thr	Leu	Phe	Leu	Ser	Ala	
			405						410					415		
Tyr	Tyr	Pro	Ser	Val	Pro	Leu	Pro	Ser	Thr	Ile	Gln	Asn	His	Val	Gly	
			420					425					430			
Asn	Thr	Ser	Gln	Asp	Asp	Ile	Ala	Thr	Ile	Leu	Ser	Lys	Val	Pro	Leu	
		435					440					445				
Glu	Asn	Asn	Tyr	Leu	Lys	Asn	Val	Val	Lys	Gln	Ile	Tyr	Gln	Asp	Leu	
	450					455					460					

Phe Gln Asp Cys His Phe Tyr His
465 470

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2298 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTTCTTTG ATTGTCTCTG CTTTAGCGTC TCTAAATCCG GTCACCATGT CGGACCCCGA	60
AGGCGAGACC TTGCGAAGCA CCTTTCCCTC TTATATGGCC GAAGGCGAGC GGCTCTACCT	120
GTGCGGGGAA TTTTCTAAAG CCGCGCAGAG CTTCAGCAAC GCTCTTTACC TTCAGGATGG	180
AGACAAGAAC TGCCTGGTTG CTCGCTCAAA GTGCTTCCTG AAGATGGGAG ACTTGAGAGAG	240
ATCCCTGAAG GATGCTGARG CTTGCTCCA GAGTGACCCA GCTTTCTGTA AGGGGATTTT	300
GCAAAAGGCT GAGACACTGT ACACCATGGG AGACTTTGAG TTTGCCTTGG TATTCTATCA	360
TCGARGCTAC AAGCTGARGC CTGATCGGGA ATTCARARTT GGCATTGAGA AAGCCCAGGA	420
AGCCATCAAC AACTCAGTGG GAAGTCCTTC TTCCATTAAG CTGGAGAACA AAGGGGACCT	480
CTCCTTCTTA AGCAAGCAGG CTGAGAATAT AAAAGCCCAG CAGAAGCCTC AGCCCATGAA	540
ACACCTCTTA CACCCACCA AGGGAGAGCC CAAGTGGAAG GCCTCGCTCA AGAGTGAGAA	600
GAAGTGTCCG CAGCTTCTGG GGGAGCTCTA CGTGGACAAA GAGTATTTGG AGAAGCTCCT	660
ATTGGATGAA GACCTGATCA AAGGCACCAT GAAGGGCGGC CTGACTGTGG AGGACCTCAT	720
CATGACGGGC ATCAACTACC TGGATACTCA CAGCAACTTC TGGAGGCAGC AGAAGCCGAT	780
CTACGCCAGG GAGCGGGACC GGAAGCTGAT GCAAGAGAAA TGGCTGCGGG ACCACAAACG	840
CCGTCCCTCA CAGACAGCCC ATTACATCCT CAAGAGCCTG GAGGACATTG ATATGTTGCT	900
CACAAGTGGC AGTGCTGAAG GGAGTCTTCA GAAAGCTGAG AAAGTGCTGA AGAAGGTACT	960
GGAATGGAAC AAGGAAGAGG TACCCAACAA GGATGAACTG GTTGGAAGT TGTATAGCTG	1020
CATAGGGAAT GCCCAGATTG AGCTGGGGCA GATGGAGGCA GCCCTGCAGA GCCACAGAAA	1080
GGACYTGGAG ATCGCCAAGG AATATGACCT TCCTGATGCA AAATCGAGAG CCCTTGACAA	1140
CATTGGCAGA GTTTTTGCCA GAGTTGGGAA ATTCCAGCAA GCCATTGACA CGTGGGAAGA	1200
AAAGATCCCT CTGGCAAAAA CCACCTGGA GAAGACCTGG CTGTTCCACG AGATCGGCCG	1260

CTGCTACTTG GAGCTGGACC AGGCCTGGCA GGCCGAGAAT TATGGCGAGA AGTCCCAGCA 1320

GTGTGCCGAG GAGGAAGGGG ACATTGAGTG GCAACTGAAT GCCAGTGTTT TGGTGGCCCA 1380

GGCACAAGTG AAGCTGAGAG ACTTCGAGTC AGCCGTGAAC AATTTTGAGA AGGCCCTGGA 1440

GAGAGCAAAG CTTGTGCATA ACAACGAGGC GCAGCAGGCC ATCATCAGTG CCTTGACGA 1500

TGCCAACAAG GGTATCATCA GAGAACTGAG GAAAACCAAC TACGTGGAGA ATCTCAAAGA 1560

AAAAAGCGAG GGAGAAGCTT CACTGTATGA AGATAGAATA ATAACAAGAG AGAAGGACAT 1620

GAGGAGAGTG AGAGATGAGC CCGAGAAGGT GGTGAAGCAG TGGGACCATA GTGAGGATGA 1680

GAAAGAGACA GATGAGGACG ATGAGGCTTT TGGGGAAGCT CTGCAGAGCC CAGCAAGCGG 1740

AAAGCAGAGT GTGGAAGCAG GAAAAGCCAG AAGCGATTTG GGAGCAGTTG CCAAGGGCCT 1800

GTCAGGAGAA TTAGGCACAA GATCAGGAGA AACAGGCAGG AAGCTACTAG AAGCTGGCAG 1860

AAGAGAGTCA AGAGAAATTT ATAGGAGGCC TTCGGGAGAA TTAGAGCAAA GACTCTCAGG 1920

AGAATTCAGC AGACAGGAAC CAGAAGAACT AAAGAACTT TCAGAAGTGG GCAGAAGAGA 1980

SCCAGAAGAA YTGGGAAAAA CACAATTTGG AGAAATAGGA GAAACGAAAA AAACAGGAAA 2040

TGAGATGGAA AAGGAATATG AATGAAGCCA TCGGTAGAGA TGAGGATCAG GAAGCTGGTG 2100

TTCAGAGGGA TCATGGGATT TTATTAACT GGATTTTCAA GCGATTTGTC TGTTATAGGA 2160

AAAATGAGGG TTTTACTTYT GCTGCTTTCC ATCACTATTT TGCCATTAAA TAGGTGTCTT 2220

TCACTCTTGC MAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2280

AAAAAAAAAA AAAAAAAAAA 2298

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Ser Asp Pro Glu Gly Glu Thr Leu Arg Ser Thr Phe Pro Ser Tyr
1 5 10 15

Met Ala Glu Gly Glu Arg Leu Tyr Leu Cys Gly Glu Phe Ser Lys Ala
20 25 30

Ala Gln Ser Phe Ser Asn Ala Leu Tyr Leu Gln Asp Gly Asp Lys Asn
35 40 45

Cys Leu Val Ala Arg Ser Lys Cys Phe Leu Lys Met Gly Asp Leu Glu

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50					55					60					
Arg	Ser	Leu	Lys	Asp	Ala	Glu	Ala	Ser	Leu	Gln	Ser	Asp	Pro	Ala	Phe
65					70					75					80
Cys	Lys	Gly	Ile	Leu	Gln	Lys	Ala	Glu	Thr	Leu	Tyr	Thr	Met	Gly	Asp
			85						90					95	
Phe	Glu	Phe	Ala	Leu	Val	Phe	Tyr	His	Arg	Xaa	Tyr	Lys	Leu	Xaa	Pro
			100					105					110		
Asp	Arg	Glu	Phe	Xaa	Xaa	Gly	Ile	Gln	Lys	Ala	Gln	Glu	Ala	Ile	Asn
		115					120					125			
Asn	Ser	Val	Gly	Ser	Pro	Ser	Ser	Ile	Lys	Leu	Glu	Asn	Lys	Gly	Asp
		130					135					140			
Leu	Ser	Phe	Leu	Ser	Lys	Gln	Ala	Glu	Asn	Ile	Lys	Ala	Gln	Gln	Lys
145					150					155					160
Pro	Gln	Pro	Met	Lys	His	Leu	Leu	His	Pro	Thr	Lys	Gly	Glu	Pro	Lys
				165					170					175	
Trp	Lys	Ala	Ser	Leu	Lys	Ser	Glu	Lys	Thr	Val	Arg	Gln	Leu	Leu	Gly
			180					185					190		
Glu	Leu	Tyr	Val	Asp	Lys	Glu	Tyr	Leu	Glu	Lys	Leu	Leu	Leu	Asp	Glu
		195					200					205			
Asp	Leu	Ile	Lys	Gly	Thr	Met	Lys	Gly	Gly	Leu	Thr	Val	Glu	Asp	Leu
		210					215					220			
Ile	Met	Thr	Gly	Ile	Asn	Tyr	Leu	Asp	Thr	His	Ser	Asn	Phe	Trp	Arg
225							230					235			240
Gln	Gln	Lys	Pro	Ile	Tyr	Ala	Arg	Glu	Arg	Asp	Arg	Lys	Leu	Met	Gln
				245					250					255	
Glu	Lys	Trp	Leu	Arg	Asp	His	Lys	Arg	Arg	Pro	Ser	Gln	Thr	Ala	His
			260					265					270		
Tyr	Ile	Leu	Lys	Ser	Leu	Glu	Asp	Ile	Asp	Met	Leu	Leu	Thr	Ser	Gly
		275					280					285			
Ser	Ala	Glu	Gly	Ser	Leu	Gln	Lys	Ala	Glu	Lys	Val	Leu	Lys	Lys	Val
		290					295					300			
Leu	Glu	Trp	Asn	Lys	Glu	Glu	Val	Pro	Asn	Lys	Asp	Glu	Leu	Val	Gly
305							310					315			320
Asn	Leu	Tyr	Ser	Cys	Ile	Gly	Asn	Ala	Gln	Ile	Glu	Leu	Gly	Gln	Met
				325					330					335	
Glu	Ala	Ala	Leu	Gln	Ser	His	Arg	Lys	Asp	Leu	Glu	Ile	Ala	Lys	Glu
			340					345					350		
Tyr	Asp	Leu	Pro	Asp	Ala	Lys	Ser	Arg	Ala	Leu	Asp	Asn	Ile	Gly	Arg
		355					360					365			

Val Phe Ala Arg Val Gly Lys Phe Gln Gln Ala Ile Asp Thr Trp Glu
 370 375 380
 Glu Lys Ile Pro Leu Ala Lys Thr Thr Leu Glu Lys Thr Trp Leu Phe
 385 390 395 400
 His Glu Ile Gly Arg Cys Tyr Leu Glu Leu Asp Gln Ala Trp Gln Ala
 405 410 415
 Gln Asn Tyr Gly Glu Lys Ser Gln Gln Cys Ala Glu Glu Glu Gly Asp
 420 425 430
 Ile Glu Trp Gln Leu Asn Ala Ser Val Leu Val Ala Gln Ala Gln Val
 435 440 445
 Lys Leu Arg Asp Phe Glu Ser Ala Val Asn Asn Phe Glu Lys Ala Leu
 450 455 460
 Glu Arg Ala Lys Leu Val His Asn Asn Glu Ala Gln Gln Ala Ile Ile
 465 470 475 480
 Ser Ala Leu Asp Asp Ala Asn Lys Gly Ile Ile Arg Glu Leu Arg Lys
 485 490 495
 Thr Asn Tyr Val Glu Asn Leu Lys Glu Lys Ser Glu Gly Glu Ala Ser
 500 505 510
 Leu Tyr Glu Asp Arg Ile Ile Thr Arg Glu Lys Asp Met Arg Arg Val
 515 520 525
 Arg Asp Glu Pro Glu Lys Val Val Lys Gln Trp Asp His Ser Glu Asp
 530 535 540
 Glu Lys Glu Thr Asp Glu Asp Asp Glu Ala Phe Gly Glu Ala Leu Gln
 545 550 555 560
 Ser Pro Ala Ser Gly Lys Gln Ser Val Glu Ala Gly Lys Ala Arg Ser
 565 570 575
 Asp Leu Gly Ala Val Ala Lys Gly Leu Ser Gly Glu Leu Gly Thr Arg
 580 585 590
 Ser Gly Glu Thr Gly Arg Lys Leu Leu Glu Ala Gly Arg Arg Glu Ser
 595 600 605
 Arg Glu Ile Tyr Arg Arg Pro Ser Gly Glu Leu Glu Gln Arg Leu Ser
 610 615 620
 Gly Glu Phe Ser Arg Gln Glu Pro Glu Glu Leu Lys Lys Leu Ser Glu
 625 630 635 640
 Val Gly Arg Arg Xaa Pro Glu Glu Leu Gly Lys Thr Gln Phe Gly Glu
 645 650 655
 Ile Gly Glu Thr Lys Lys Thr Gly Asn Glu Met Glu Lys Glu Tyr Glu
 660 665 670

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```
GGAAGAGCCA CCATCCCTGC CCCCGTTTTC CCACCGGGGA GTCTGTACAG AGATTTTCTCT      60
ACGTTTTTAT TTTTTCCTC AGAGGGATGG GATTGGGGAG GAGGGGATGG GCAGCGGAGG      120
GTTGGGGGCA TGGTCTGCAG GCTCATCTGT GTCCGCCTTT CACTCCACTA ATGCTGTCTC      180
AGTGTTTTCT CTCTCTCTCT TTCGAGCTTG CACTCCGGTA CCCGACCCGG CGCCCTGGCC      240
CATCCCATGC CGGGGGGCCA GTGGAAAGAA GACAGGCCGT CCAGCCCGTG CCCGCCTGCG      300
GCGGGGGCAC CCAGCAAGCC CGCCCACCGC CCGCTGCCTC ACCTGCTTCG CCACAGACTC      360
TTGTTCCCAG CCCCTTGGGG CCTCCGTGTT TGGGGTGGGG GAGCTGCTTA GAGACTGTGC      420
CCGTCTCGG CCCCCACCC TGAAGTGCCA GCACCACCAG CACCAGATCT TCCGCCGCCA      480
CACCGCATTG AGGACACGCC GGCCGGGCCG CTTCGTCTCA AGTTGTATAA AGTTGTCTCC      540
GTGTCCCCTC CTCCCTCTGC CCCCAGTGTT TCTTCTGATT TTTTTTCCC CTTTCCCTCC      600
CTCCCTCTCC GCATTCTTCC CTTGGTTCAG CACAGGTAAA ACGGTTCCTC TCCCTCCCTG      660
CCTTCATGGA TCACCAGCTC ACGTCATGTT GCCTTCTCTT TTCTTTGTGT GTGTGTTTAT      720
TTAAGTTATT TTTCTTCCTC CTCTCCCTTT TCTTTTGGC CCTCCCTCCC TCCCTCTTCT      780
GCCATGTAAC TGGAGGATGT GCTATGAGTT TGCAAACAGC TGGACTGTCA GGCTGCTTTT      840
TTTTCCAGAT GTTCTTCTTC TGCTTCCCCT TCCCCTCCTC TCCCCTCCTT TTCCTTCCTT      900
CCTTCCTTTC CTTGGAGCAC TGAGCACCAT TTGGAAGCTT GAGAGAAACC AAAATTAAAG      960
AGAGAAAGAG AGAGCGTGCA CGCTCCTGCT TTGTCAAAAA AAAAAAAAAA      1010
```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Gly	Ser	Gly	Gly	Leu	Gly	Ala	Trp	Ser	Ala	Gly	Ser	Ser	Val	Ser	
1				5					10					15		
Ala	Phe	His	Ser	Thr	Asn	Ala	Val	Ser	Val	Phe	Ser	Leu	Ser	Leu	Phe	
			20					25					30			
Arg	Ala	Cys	Thr	Pro	Val	Pro	Asp	Pro	Ala	Pro	Trp	Pro	Ile	Pro	Cys	
		35					40					45				
Arg	Gly	Ala	Ser	Gly	Lys	Lys	Thr	Gly	Arg	Pro	Ala	Arg	Ala	Arg	Leu	
	50					55					60					
Arg	Arg	Gly	His	Pro	Ala	Ser	Pro	Pro	Thr	Ala	Arg	Cys	Leu	Thr	Cys	
65					70					75					80	
Phe	Ala	Thr	Asp	Ser	Cys	Ser	Gln	Pro	Leu	Gly	Ala	Ser	Val	Phe	Gly	
				85					90					95		
Val	Gly	Glu	Leu	Leu	Arg	Asp	Cys	Ala	Arg	Pro	Arg	Pro	Pro	Thr	Leu	
			100					105					110			
Lys	Cys	Gln	His	His	Gln	His	Gln	Ile	Phe	Arg	Arg	His	Thr	Ala	Leu	
		115					120					125				
Arg	Thr	Arg	Arg	Pro	Gly	Arg	Phe	Val	Ser	Ser	Cys	Ile	Lys	Leu	Ser	
	130					135					140					
Pro	Cys	Pro	Leu	Leu	Pro	Leu	Pro	Pro	Val	Phe	Leu	Leu	Ile	Phe	Phe	
145					150					155					160	
Ser	Pro	Phe	Pro	Pro	Ser	Leu	Ser	Ala	Phe	Phe	Pro	Trp	Phe	Ser	Thr	
				165					170					175		
Gly	Lys	Thr	Val	Pro	Leu	Pro	Pro	Cys	Leu	His	Gly	Ser	Pro	Ala	His	
			180					185					190			
Val	Met	Leu	Pro	Ser	Leu	Phe	Phe	Val	Cys	Val	Phe	Ile				
		195					200					205				

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTTYGCTCA TCAACCTCAT TATAGAACAT ATGATTTGTG ATACAGATCC TGAAGTTGGA	60
GGAGCAGTCC AGCTTATGGG CCTGCTTCGA ACTTTAGTTG ACCCAGAGAA CATGCTAGCC	120
ACTGCCMATA AAACASAAAA GACTGAATTT CTGGGTTTCT TCTACAAGCA CTGTATGCAT	180

GTTCTCWCTG CTCCTTTACT AGCAAATACA ACAGAAGACA AACCTAGTAA AGATGATTTT	240
CAGACTGCCC AACTATTGGC ACTTGTATTG GAATTGTAA CATTTTGTGT GGAGCACCAT	300
ACCTACCACA TAAAGAACTA CATTATTAAT AAGGATATCC TCCGGAGAGT GCTAGTTCTT	360
ATGGCCTCGA AGCATGCTTT CTTGGCATTG TGTGCCCTTC GTTTTAAAAG AAAGATTATT	420
GGATTAAAAG ATGAGTTTTA CAACCGCTAC ATAATGAAAA GTTTTTTGTG TGAACCAGTA	480
GTGAAAGCAT TTCTCAACAA TGGATCCCGC TACAATCTGA TGAACCTGTC CATAATAGAG	540
ATGTTTGAAT TTATTAGAGT GGAAGATATA AAATCATTA C TGCTCATGT AATTGAAAAT	600
TACTGGAAAG CACTGGAAGA TGTAGATTAT GTACAGACAT TTAAAGGATT AAAACTGAGA	660
TTTGAACAAC AAAGAGAAAG GCAAGATAAT CCCAACTTG ACAGTATGCG TTCCATTTTG	720
AGGAATCACA GATATCGAAG AGATGCCAGA AACTAGAAG ATGAAGAAGA GATGTGGTTT	780
AACACAGATG AAGATGACAT GGAAGATGGA GAAGCTGTAG TGTCTCCATC TGACAAAAC	840
AAAAATGATG ATGATATTAT GGATCCAATA AGTAAATTCA TGGAAAGGAA GAAATTAAAA	900
GAAAGTGAGG AAAAGGAAGT GCTTCTGAAA ACAAACCTTT CTGGACGGCA GAGCCCAAGT	960
TTCAAGCTTT CCCTGTCCAG TGGAACGAAG ACTAACCTCA CCAGCCAGTC ATCTACAACA	1020
AATCTGCCTG GTTCTCCGGG ATCACCTGGA TCCCAGGAT CTCCAGGCTC TCCTGGATCC	1080
GTACCTAAAA ATACATCTCA GACGGCAGCT ATTACTACAA AGGGAGGCCT CGTGGGTCTG	1140
GTAGATTATC CTGATGATGA TGAAGATGAT GATGAGGATG AAGATAAGGA AGATACGTTA	1200
CCATTGTCAA AGAAAGCAAA ATTTGATTCA TAATAATGGC AACGGCCTAG GATCAGTACC	1260
TGTTGAAAAA AACTGGTTCT CCACCCCTCC CCCATACAAA ATCCACAAAA AAGCGCAGTG	1320
GTCTCTTG TG AATGACTGAC ACAGATCAGC CTCTTACACT TGA CTCTGTC TCATCAAGTG	1380
CCAATTCAAT GGAGCAGGAG GAGGGGATAT CATATATTTA GGGGAAAGAC TTAAGCCTTT	1440
GAGCTCTCCA GCTTGGACCA CACATTGCCC TTTTCTCAGG GAAGGAAATG GAAACAAAAA	1500
GCCAACAGGG CAGGGGTTTT GTAAGTGGAA CTCTGGATTG ACTGGTCAGT TGCTACAATC	1560
AGAATATGCT TTCTTGACC ATGTTTGAGA CTCAGAAGAA TGGCCTTTCT GCCATAATTC	1620
TTCCTAGTC AAGAATGCCA GCAGTTTCTT TGTATAAAGA GACCTGCCTT TAAATCATA	1680
CATTCTGAAC ATTTTAGTCA AGCTACAACA GTTTGGAAA ACCTCTGTGG GGGAGGGGCG	1740
AGTATAAAGT TTTCTCTTT TTTAACTGTT CCCTTTGCCC TTCAAACCTGC AGATATTTTT	1800
TTTTTTAAGT GGGGACTTCT CCCTACTTGA TTAAAGATTG AGTGGAATTC TAGATGTGGT	1860

CATTGTGTC ATAATTTTTT TGTTTTATTT TGTTTTGGAT TTTTTTTTTC CTCCCCTGAG 1920
 TGTATGCTTA GTTGTGAGT ATATATATTT GGGACCATTA AAACCTTTTTT TGATGTAATA 1980
 TAACCTAACG TTGTGCTGGT ACCTGTTTTA CCATGTGTAA TTTTGTCTT ACATCACAGT 2040
 TCTTAATTTG TTTAGAGTTT TATGAAAGAT GGTATAGTTT TTATTGACAA AAGCAAAGTA 2100
 ATCTTACAAC TATGTGCATA CAAAAGCAAT ACTATTTTGT GACTAAATAT TTTATATTAA 2160
 AATTTACATC AGCAACTGTC TTGAGAATTC AGGGAAATAG AATGGAATTT AAAACTTCAA 2220
 CAGTTTTGTT AAATCTAGAA ACATGAAATT RGTATTCCAA AGAGATTCTG AAATTTCTTT 2280
 TCTKGGGGAA ATGACGGTAC ATTAAATCAA AATTGRGGAT GGATGATTTA AAAACATTTG 2340
 ACTTTTTAAT AATAAAAAGA AAAGTGAAGA GTAAGAGAAA TTGTAAAAAA AAAAAAAAAA 2400
 AAAAAAAAAA 2409

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met	Ile	Cys	Asp	Thr	Asp	Pro	Glu	Leu	Gly	Gly	Ala	Val	Gln	Leu	Met
1				5					10					15	
Gly	Leu	Leu	Arg	Thr	Leu	Val	Asp	Pro	Glu	Asn	Met	Leu	Ala	Thr	Ala
			20					25					30		
Xaa	Lys	Thr	Xaa	Lys	Thr	Glu	Phe	Leu	Gly	Phe	Phe	Tyr	Lys	His	Cys
			35					40					45		
Met	His	Val	Leu	Xaa	Ala	Pro	Leu	Leu	Ala	Asn	Thr	Thr	Glu	Asp	Lys
			50				55					60			
Pro	Ser	Lys	Asp	Asp	Phe	Gln	Thr	Ala	Gln	Leu	Leu	Ala	Leu	Val	Leu
65					70					75					80
Glu	Leu	Leu	Thr	Phe	Cys	Val	Glu	His	His	Thr	Tyr	His	Ile	Lys	Asn
				85					90					95	
Tyr	Ile	Ile	Asn	Lys	Asp	Ile	Leu	Arg	Arg	Val	Leu	Val	Leu	Met	Ala
			100					105					110		
Ser	Lys	His	Ala	Phe	Leu	Ala	Leu	Cys	Ala	Leu	Arg	Phe	Lys	Arg	Lys
			115					120				125			
Ile	Ile	Gly	Leu	Lys	Asp	Glu	Phe	Tyr	Asn	Arg	Tyr	Ile	Met	Lys	Ser

130		135		140
Phe Leu Phe Glu Pro Val Val Lys Ala Phe Leu Asn Asn Gly Ser Arg				
145		150		155 160
Tyr Asn Leu Met Asn Ser Ala Ile Ile Glu Met Phe Glu Phe Ile Arg				
	165		170	175
Val Glu Asp Ile Lys Ser Leu Thr Ala His Val Ile Glu Asn Tyr Trp				
	180		185	190
Lys Ala Leu Glu Asp Val Asp Tyr Val Gln Thr Phe Lys Gly Leu Lys				
	195		200	205
Leu Arg Phe Glu Gln Gln Arg Glu Arg Gln Asp Asn Pro Lys Leu Asp				
	210		215	220
Ser Met Arg Ser Ile Leu Arg Asn His Arg Tyr Arg Arg Asp Ala Arg				
	225		230	235 240
Thr Leu Glu Asp Glu Glu Glu Met Trp Phe Asn Thr Asp Glu Asp Asp				
	245		250	255
Met Glu Asp Gly Glu Ala Val Val Ser Pro Ser Asp Lys Thr Lys Asn				
	260		265	270
Asp Asp Asp Ile Met Asp Pro Ile Ser Lys Phe Met Glu Arg Lys Lys				
	275		280	285
Leu Lys Glu Ser Glu Glu Lys Glu Val Leu Leu Lys Thr Asn Leu Ser				
	290		295	300
Gly Arg Gln Ser Pro Ser Phe Lys Leu Ser Leu Ser Ser Gly Thr Lys				
	305		310	315 320
Thr Asn Leu Thr Ser Gln Ser Ser Thr Thr Asn Leu Pro Gly Ser Pro				
	325		330	335
Gly Ser Pro Gly Ser Pro Gly Ser Pro Gly Ser Pro Gly Ser Val Pro				
	340		345	350
Lys Asn Thr Ser Gln Thr Ala Ala Ile Thr Thr Lys Gly Gly Leu Val				
	355		360	365
Gly Leu Val Asp Tyr Pro Asp Asp Asp Glu Asp Asp Asp Glu Asp Glu				
	370		375	380
Asp Lys Glu Asp Thr Leu Pro Leu Ser Lys Lys Ala Lys Phe Asp Ser				
	385		390	395 400

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 951 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCCAGGCAGG GTGTGGGGGC AGCTGTGCCA ATCTACCTCA CAGGCCCACC CCCTGCCGGG 60
CATGCCGTGG GATCATGGGC AGGGAAGGCT CTGGGGGTCTG GAGACACCGC TGCTTAGCAC 120
CCCCAGCCAG AACACCCTGA GGGTCTCGGG GCTCTGGAGA GAGTGGGGCG GGAGGAAGAA 180
TTGGCACCTT CCTAGGGAAG GAGACGAGCG CTTCGCCTTG ATTCTCCGAG AAGCCTCCGA 240
GAAGTGCTTT AAGTGTGTTT GCATGCSCCA GGCGGTGGGC AGCGGGGGCC TGTCCARCCC 300
TCTCCCGCCA TCCTTCCCCA AGTGACGTCC ACTGCCTTGT CACCAGCGAC CTGCCTGTCA 360
TGCCACCCC CTGAGGAAGC ATGGGGACCC TAACACCCTG GTGCCCTGCA CCAGACAGGC 420
CGTGGTCAGG CCCAGGCCAC CGGCCGGGTT CTGCCACARC TTCCACGTG CTTGCTGACA 480
TGCSTGTGCC TGTGTGTGGT GTCTGTTGCT GTGTCGTGAA ACTGTGACCA TCACTCAGTC 540
CAAACAAGTG AGTGGCCCTS GAGGCCACAG TTATGCAACT TTCAGTGTGT GTCATAACGA 600
CGTCACTGCT TTTTAACTC GATAACTCTT TATTTTAGTA AAATGCCAG GAGTCCTGGA 660
AGCTACGCGG ACTTGAGAG GTTTTATTTT TTGGCCTTAG AATCTGCAGA AATTAGGAGG 720
CACCGAGCCC AGCGCAGCAG CCTCGGACCC GGATTGCGTT TGCCCTTAGCG GATATGTTTA 780
TACAGATGAA TATAAAATGT TTTTCTCTT GGGCTTTTGT CTTCTTTTTT CCCCCCTTC 840
TCACCTTCCC TTCTCCCTGA CCCCACCCC CAAAAAGCT ACTTCTTCAT TCCGTGGTAC 900
GATTATTTTT TTTAACTAAA GGAAGATAAA ATTCTAAAAA AAAAAAAAAA A 951

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Pro Trp Asp His Gly Gln Gly Arg Leu Trp Gly Ser Glu Thr Pro
1 5 10 15
Leu Leu Ser Thr Pro Ser Gln Asn Thr Leu Arg Val Ser Gly Leu Trp
20 25 30
Arg Glu Trp Gly Gly Arg Lys Asn Trp His Leu Pro Arg Glu Gly Asp
35 40 45

Glu Arg Phe Ala Leu Ile Leu Arg Glu Ala Ser Glu Lys Cys Phe Lys
50 55 60

Cys Val Cys Met Xaa Gln Ala Val Gly Ser Gly Gly Leu Ser Xaa Pro
65 70 75 80

Leu Pro Pro Ser Phe Pro Lys
85

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1899 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCCGCTTGT GTCCACGGGA CGCGGGCGGA TCTTCTCCGG CCATGAGGAA GCCAGCCGCT	60
GGCTTCCTTC CCTCACTCCT GAAGGTGCTG CTCCTGCCTC TGGCACCTGC CGCAGCCCAG	120
GATTCGACTC AGGCCTCCAC TCCAGGCAGC CCTCTCTCTC CTACCGAATA CGAACGCTTC	180
TTCGCACTGC TGACTCCAAC CTGGAAGGCA GAGACTACCT GCCGTCTCCG TGCAACCCAC	240
GGCTGCCGGA ATCCCACACT CGTCCAGCTG GACCAATATG AAAACCACGG CTTAGTGCCC	300
GATGGTGCTG TCTGCTCCAA CCTCCCTTAT GCCTCCTGGT TTGAGTCTTT CTGCCAGTTC	360
ACTCACTACC GTTGCTCCAA CCACGTCTAC TATGCCAAGA GAGTCCTGTG TTCCAGCCA	420
GTCTCTATTC TCTCACCTAA CACTCTCAAG GAGATAGAAG CTTCACTGA AGTCTCACCC	480
ACCACGATGA CCTCCCCCAT CTCACCCAC TTCACAGTGA CAGAACGCCA GACCTTCCAG	540
CCCTGGCCTG AGAGGCTCAG CAACAACGTG GAAGAGCTCC TACAATCCTC CTTGTCCCTG	600
GGAGGCCAGG AGCAAGCGCC AGAGCACAAG CAGGAGCAAG GAGTGGAGCA CAGGCAGGAG	660
CCGACACAAG AACACAAGCA GGAAGAGGGG CAGAAACAGG AAGAGCAAGA AGAGGAACAG	720
GAAGAGGAGG GAAAGCAGGA AGAAGGACAG GGGACTAAGG AGGGACGGGA GGCTGTGTCT	780
CAGCTGCAGA CAGACTCAGA GCCCAAGTTT CACTCTGAAT CTCTATCTTC TAACCTTCC	840
TCTTTTGCTC CCCGGGTACG AGAAGTAGAG TCTACTCCTA TGATAATGGA GAACATCCAG	900
GAGCTCATTC GATCAGCCCA GGAAATAGAT GAAATGAATG AAATATATGA TGAGAACTCC	960
TACTGGAGAA ACCAAAACCC TGGCAGCCTC CTGCAGCTGC CCCACACAGA GGCCTTGCTG	1020
GTGCTGTGCT ATTCGATCGT GGAGAATACC TGCATCATAA CCCCCACAGC CAAGGCCTGG	1080

AAGTACATGG AGGAGGAGAT CCTTG GTTTC GGAAGTCGG TCTGTGACAG CCTTGGGCGG 1140
 CGACACATGT CTACCTGTGC CCTCTGTGAC TTCTGCTCCT TGAAGCTGGA GCAGTGCCAC 1200
 TCAGAGGCCA GCCTGCAGCG GCAACAATGC GACACCTCCC ACAAGACTCC CTTTGTTCAGC 1260
 CCCTTGCTTG CCTCCCAGAG CCTGTCCATC GGCAACCAGG TAGGGTCCCC AGAATCAGGC 1320
 CGCTTTTACG GGCTGGATTT GTACGGTGGG CTCCACATGG ACTTCTGGTG TGCCCGGCTT 1380
 GCCACGAAAG GCTGTGAAGA TGTCCGAGTC TCTGGGTGGC TCCAGACTGA GTTCCTTAGC 1440
 TTCCAGGATG GGGATTTCCC TACCAAGATT TGTGACACAG ACTATATCCA GTACCCAAAC 1500
 TACTGTTTCT TCAAAAGCCA GCAGTGTCTG ATGAGAAACC GCAATCGGAA GGTGTCCCGC 1560
 ATGAGATGTC TGCAGAATGA GACTTACAGT GCGCTGAGCC TGGCAAAAGT GAGGACGTTG 1620
 TGCTTTTCGAT GGAGCCAGGA GTTCAGCACC TTGACTCTAG GCCAGTTCGG ATGAGCTKGS 1680
 GTTTATTTTG CCCACACCCC AGCCCAACCT GCCCASGTTT TCTATTGTTT TGAGACCCCA 1740
 TTGCTTTCAG GCTGCCCCCTT CTGGGTCTGT TACTCGGCCC CTAMTCACAT TTCCTTGGGT 1800
 TGGAGCAACA GTCCCAGAGA GGGCCACGGT GGGAGCTGCG CCCTCCTTAA AAGATGACTT 1860
 TACATAAAAT GTTGATCTTC AAAAAAAAAA AAAAAAAAAA 1899

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Arg	Lys	Pro	Ala	Ala	Gly	Phe	Leu	Pro	Ser	Leu	Leu	Lys	Val	Leu
1				5				10					15		
Leu	Leu	Pro	Leu	Ala	Pro	Ala	Ala	Ala	Gln	Asp	Ser	Thr	Gln	Ala	Ser
			20					25					30		
Thr	Pro	Gly	Ser	Pro	Leu	Ser	Pro	Thr	Glu	Tyr	Glu	Arg	Phe	Phe	Ala
			35					40					45		
Leu	Leu	Thr	Pro	Thr	Trp	Lys	Ala	Glu	Thr	Thr	Cys	Arg	Leu	Arg	Ala
			50				55				60				
Thr	His	Gly	Cys	Arg	Asn	Pro	Thr	Leu	Val	Gln	Leu	Asp	Gln	Tyr	Glu
65					70					75				80	
Asn	His	Gly	Leu	Val	Pro	Asp	Gly	Ala	Val	Cys	Ser	Asn	Leu	Pro	Tyr
			85					90					95		

Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser
 100 105 110
 Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser
 115 120 125
 Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu Ala Ser Ala Glu Val
 130 135 140
 Ser Pro Thr Thr Met Thr Ser Pro Ile Ser Pro His Phe Thr Val Thr
 145 150 155 160
 Glu Arg Gln Thr Phe Gln Pro Trp Pro Glu Arg Leu Ser Asn Asn Val
 165 170 175
 Glu Glu Leu Leu Gln Ser Ser Leu Ser Leu Gly Gly Gln Glu Gln Ala
 180 185 190
 Pro Glu His Lys Gln Glu Gln Gly Val Glu His Arg Gln Glu Pro Thr
 195 200 205
 Gln Glu His Lys Gln Glu Glu Gly Gln Lys Gln Glu Glu Gln Glu Glu
 210 215 220
 Glu Gln Glu Glu Glu Gly Lys Gln Glu Glu Gly Gln Gly Thr Lys Glu
 225 230 235 240
 Gly Arg Glu Ala Val Ser Gln Leu Gln Thr Asp Ser Glu Pro Lys Phe
 245 250 255
 His Ser Glu Ser Leu Ser Ser Asn Pro Ser Ser Phe Ala Pro Arg Val
 260 265 270
 Arg Glu Val Glu Ser Thr Pro Met Ile Met Glu Asn Ile Gln Glu Leu
 275 280 285
 Ile Arg Ser Ala Gln Glu Ile Asp Glu Met Asn Glu Ile Tyr Asp Glu
 290 295 300
 Asn Ser Tyr Trp Arg Asn Gln Asn Pro Gly Ser Leu Leu Gln Leu Pro
 305 310 315 320
 His Thr Glu Ala Leu Leu Val Leu Cys Tyr Ser Ile Val Glu Asn Thr
 325 330 335
 Cys Ile Ile Thr Pro Thr Ala Lys Ala Trp Lys Tyr Met Glu Glu Glu
 340 345 350
 Ile Leu Gly Phe Gly Lys Ser Val Cys Asp Ser Leu Gly Arg Arg His
 355 360 365
 Met Ser Thr Cys Ala Leu Cys Asp Phe Cys Ser Leu Lys Leu Glu Gln
 370 375 380
 Cys His Ser Glu Ala Ser Leu Gln Arg Gln Gln Cys Asp Thr Ser His
 385 390 395 400

Lys Thr Pro Phe Val Ser Pro Leu Leu Ala Ser Gln Ser Leu Ser Ile
 405 410 415
 Gly Asn Gln Val Gly Ser Pro Glu Ser Gly Arg Phe Tyr Gly Leu Asp
 420 425 430
 Leu Tyr Gly Gly Leu His Met Asp Phe Trp Cys Ala Arg Leu Ala Thr
 435 440 445
 Lys Gly Cys Glu Asp Val Arg Val Ser Gly Trp Leu Gln Thr Glu Phe
 450 455 460
 Leu Ser Phe Gln Asp Gly Asp Phe Pro Thr Lys Ile Cys Asp Thr Asp
 465 470 475 480
 Tyr Ile Gln Tyr Pro Asn Tyr Cys Ser Phe Lys Ser Gln Gln Cys Leu
 485 490 495
 Met Arg Asn Arg Asn Arg Lys Val Ser Arg Met Arg Cys Leu Gln Asn
 500 505 510
 Glu Thr Tyr Ser Ala Leu Ser Leu Ala Lys Val Arg Thr Leu Cys Phe
 515 520 525
 Arg Trp Ser Gln Glu Phe Ser Thr Leu Thr Leu Gly Gln Phe Gly
 530 535 540

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGACCTTCCC AGCAATATGC ATCTTGCACG TCTGGTCGGC TCCTGCTCCC TCCTTCTGCT	60
ACTGGGGGCC CTGTCTGGAT GGGCGGCCAG CGATGACCCC ATTGAGAAGG TCATTGAAGG	120
GATCAACCGA GGGCTGAGCA ATGCAGAGAG AGAGGTGGGC AAGGCCCTGG ATGGCATCAA	180
CAGTGAATC ACGCATGCCG GAAGGGAAGT GGAGAAGGTT TTCAACGGAC TTAGCAACAT	240
GGGGAGCCAC ACCGGCAAGG AGTTGGACAA AGGCGTCCAG GGGCTCAACC ACGGCATGGA	300
CAAGGTTGCC CATGAGATCA ACCATGGTAT TGGACAAGCA GGAAAGGAAG CAGAGAAGCT	360
TGGCCATGGG GTCAACAACG CTGCTGGACA GGGCAACCAT CAAAGCGGAT CTTCCAGCCA	420
TCAAGGAGGG GCCACAACCA CGCCGTTAGC CTCTGGGGCC TCGGTCAACA CGCCTTTCAT	480
CAACCTTCCC GCCCTGTGGA GGAGCGTCGC CAACATCATG CCCTAAACTG GCATCCGGCC	540
TTGCTGGGAG AATAATGTCG CCGTTGTCAC ATCAGCTGAC ATGACCTGGA GGGGTGGGG	600

GTGGGGGACA GGTTCCTGAA ATCCCTGAAG GGGGTTGTAC TGGGATTTGT GAATAAACTT 660
 GATACACTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 720
 AA 722

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	Leu	1	5	10	15
Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	Lys	Val	20	25	30	
Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	Glu	Val	Gly	35	40	45	
Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	Ala	Gly	Arg	Glu	50	55	60	
Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	Gly	Ser	His	Thr	Gly	65	70	75	80
Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	Asn	His	Gly	Met	Asp	Lys	85	90	95	
Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	Gly	Gln	Ala	Gly	Lys	Glu	Ala	100	105	110	
Glu	Lys	Leu	Gly	His	Gly	Val	Asn	Asn	Ala	Ala	Gly	Gln	Gly	Asn	His	115	120	125	
Gln	Ser	Gly	Ser	Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	130	135	140	
Ala	Ser	Gly	Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	145	150	155	160
Trp	Arg	Ser	Val	Ala	Asn	Ile	Met	Pro								165			

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1240 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATGGCTTTT CTTCCTTCCT GGGTTTGTGT ACTAGTTGGT TCCTTTTCTG CTTCCTTAGC	60
AGGGACTTCC AATCTCTCAG AGACAGAGCC CCCTCTGTGG AAGGAGAGTC CTGGTCAGCT	120
CAGTGACTAC AGGGTGGAGA ACAGCATGTA CATTATTAAT CCCTGGGTAT ACCTTGAGAG	180
AATGGGGATG TATAAAATCA TATTGAATCA GACAGCCAGG TATTTTGCAA AATTGCACC	240
AGATAATGAA CAGAATATTT TATGGGGGTT GCCTCTGCAG TATGGCTGGC AATATAGGAC	300
AGGCAGATTA GCTGATCCAA CCCGAAGGAC AAAGTGTGGC TATGAATCTG GAGATCATAT	360
GTGCATCTCT GTGGACAGTT GGTGGGCTGA TTTGAATTAT TTTCTGTCTT CATTACCCTT	420
TCTTGCTGCG GTTGATTCTG GTGTAATGGG GATATCATCA GACCAAGTCA GGCTTTTGCC	480
CCCACCCAAG AATGAGAGGA AGTTTTGTTA TGATGTTTCT AGCTGTCGTT CATCCTTCCC	540
TGAGACAATG AACAAGTGGG ACACCTTTTA CCAGTATTTG CAGTCACCTT TTAGTAAGTT	600
TGATGATCTG TTGAAGTACT TATGGGCTGC ACACACTTCA ACCTTGGCAG ATAATATCAA	660
AAGTTTTGAA GACAGATATG ATTATTATTC TAAAGCAGAA GCGCATTTTG AGAGAAAGTTG	720
GGTACTGGCT GTGGATCATT TAGCTGCAGT CCTCTTTCCT ACAACCTTGA TTAGATCATA	780
TAAGTTCCAG AAGGGCATGC CACCACGAAT TCTTCTTAAT ACTGATGTAG CCCCTTTCAT	840
CAGTGACTTT ACTGCTTTTC AGAATGTAGT CCTGGTTCTT CTAAATATGC TTGACAATGT	900
GGATAAATCT ATAGGTTATC TTTGTACAGA AAAATCTAAT GTATATAGAG ATCATTCGGA	960
ATCTAGCTCT AGAAGTTATG GAAATAACTC CTGAAACATT TAACTTCAAA CTCAGGAAA	1020
TGATTAATGA ATTAAAAATG AAAAAGTCGA ACTTGACAAT CAGTAATTTT AAAAAATTAA	1080
TGTCATCATG ACCATGTAGT TTATTCCTTC TGATATTTT GATTATGCT TATTTGTAA	1140
GATCTTGATC ATGTATTAAA AACTTAAATT AAATGCATTC AAGTTAAAAA AAAAAAAAAA	1200
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1240

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met	Ala	Phe	Leu	Pro	Ser	Trp	Val	Cys	Val	Leu	Val	Gly	Ser	Phe	Ser	
1				5				10						15		
Ala	Ser	Leu	Ala	Gly	Thr	Ser	Asn	Leu	Ser	Glu	Thr	Glu	Pro	Pro	Leu	
			20					25					30			
Trp	Lys	Glu	Ser	Pro	Gly	Gln	Leu	Ser	Asp	Tyr	Arg	Val	Glu	Asn	Ser	
		35					40					45				
Met	Tyr	Ile	Ile	Asn	Pro	Trp	Val	Tyr	Leu	Glu	Arg	Met	Gly	Met	Tyr	
	50					55					60					
Lys	Ile	Ile	Leu	Asn	Gln	Thr	Ala	Arg	Tyr	Phe	Ala	Lys	Phe	Ala	Pro	
65					70					75					80	
Asp	Asn	Glu	Gln	Asn	Ile	Leu	Trp	Gly	Leu	Pro	Leu	Gln	Tyr	Gly	Trp	
				85					90					95		
Gln	Tyr	Arg	Thr	Gly	Arg	Leu	Ala	Asp	Pro	Thr	Arg	Arg	Thr	Asn	Cys	
			100					105						110		
Gly	Tyr	Glu	Ser	Gly	Asp	His	Met	Cys	Ile	Ser	Val	Asp	Ser	Trp	Trp	
		115					120					125				
Ala	Asp	Leu	Asn	Tyr	Phe	Leu	Ser	Ser	Leu	Pro	Phe	Leu	Ala	Ala	Val	
	130					135					140					
Asp	Ser	Gly	Val	Met	Gly	Ile	Ser	Ser	Asp	Gln	Val	Arg	Leu	Leu	Pro	
145					150					155					160	
Pro	Pro	Lys	Asn	Glu	Arg	Lys	Phe	Cys	Tyr	Asp	Val	Ser	Ser	Cys	Arg	
				165					170					175		
Ser	Ser	Phe	Pro	Glu	Thr	Met	Asn	Lys	Trp	Asn	Thr	Phe	Tyr	Gln	Tyr	
			180					185					190			
Leu	Gln	Ser	Pro	Phe	Ser	Lys	Phe	Asp	Asp	Leu	Leu	Lys	Tyr	Leu	Trp	
		195					200					205				
Ala	Ala	His	Thr	Ser	Thr	Leu	Ala	Asp	Asn	Ile	Lys	Ser	Phe	Glu	Asp	
	210					215					220					
Arg	Tyr	Asp	Tyr	Tyr	Ser	Lys	Ala	Glu	Ala	His	Phe	Glu	Arg	Ser	Trp	
225					230					235					240	
Val	Leu	Ala	Val	Asp	His	Leu	Ala	Ala	Val	Leu	Phe	Pro	Thr	Thr	Leu	
				245					250					255		
Ile	Arg	Ser	Tyr	Lys	Phe	Gln	Lys	Gly	Met	Pro	Pro	Arg	Ile	Leu	Leu	
			260					265					270			
Asn	Thr	Asp	Val	Ala	Pro	Phe	Ile	Ser	Asp	Phe	Thr	Ala	Phe	Gln	Asn	
		275					280					285				

Val Val Leu Val Leu Leu Asn Met Leu Asp Asn Val Asp Lys Ser Ile
 290 295 300

Gly Tyr Leu Cys Thr Glu Lys Ser Asn Val Tyr Arg Asp His Ser Glu
 305 310 315 320

Ser Ser Ser Arg Ser Tyr Gly Asn Asn Ser
 325 330

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCAGCACCAG CCGTCTGCAG CTCCGGCCGC CACTTGCGCC TCTCCAGCCT CCGCAGGCCC	60
AACCGCCGCC AGCACCATGG CCAGCACCAT TTCCGCCTAC AAGGAGAAGA TGAAGGAGCT	120
GTCGGTGCTG TCGCTCATCT GCTCCTGCTT CTACACACAG CCGCACCCCA ATACCGTCTA	180
CCAGTACGGG GACATGGAGG TGAAGCAGCT GGACAAGCGG GCCTCAGGCC AGAGCTTCGA	240
GGTCATCCTC AAGTCCCCTT CTGACCTGTC CCCAGAGAGC CCTATGCTCT CCTCCCCACC	300
CAAGAAGAAG GACACCTCCC TGGAGGAGCT GCAAAAGCGG CTGGAGGCAG CCGAGGAGCG	360
GAGGAAGACG CAGGAGGCGC AGGTGCTGAA GCAGCTGGCG GAGCGGCGCG AGCACGAGCG	420
CGAGGTGCTG CACAAGGCGC TGGAGGAGAA TAACAACCTT AGCCGCCAGG CGGAGGAGAA	480
GCTCAACTAC AAGATGGAGC TCAGCAAGGA GATCCGCGAG GCACACCTGG CCGCACTGCG	540
CGAGCGGCTG CGCGAGAAGG AGCTGCACGC GGCCGAGGTG CGCAGGAACA AGGAGCAGCG	600
AGAAGAGATG TCGGGCTAAG GGCCCGGGAC GGGCGGCGCC CATCCTGCGA CAGAACACGT	660
TCGGGTTTTG GTTTTGTTTC GTTCACCTCT GTCTAGATGC AACTTTTGTT CCTCCTCCCC	720
CACCCAGCC CCCAGCTTCA TGCTTCTCTT CCGCACTCAG CCGCCCTGCC CTGTCTCTCGT	780
GGTGAGTCGC TGACCACGGC TTCCCCTGCA GGAGCCGCCG GCGGTGAGAC GCGGTCCCTC	840
GGTGACAGACA CCAGGCCGGG CGCGGCTGGG TCCCCCGGGG GCCCTGTGAG AGAGGTGGCG	900
GTGACCGTGG TAAACCCAGG GCGGTGGCGT GGGATCGCGG GTCCTTACGC TGGGCTGTCT	960
GGTCAGCACG TGCAGGTCAG GGCAGGTCCT CTGAGCCGGC GCCCCTGGCC AGCAGGCGAG	1020
GCTACAGTAC CTGCTGTCTT TCCAGGGGGA AGGGGCTCCC CATGAGGGAG GGGCGACGGG	1080

GGAGGGGGGT GATGGTGCCT GGGAGCCTGC GTGTGCAGCC GGTGCTTGTT GAACTGGCAG 1140
GCGGGTGGGT GGGGGCTGCA GCTTTCCTTA ATGTGGTTGC ACAGGGGTCC TCTGAGACCA 1200
CCTGGCGTGA GGTGGACACC CTGGGCCTTC CTGGAAGCCT GCAGTTGGGG GCCTGCCCTG 1260
AGTCTGCTGG GGAGTGGGCA TTCTCTGCCA GGGACCCATG AGCAGGCTGC ATGGTCTAGA 1320
GGTTGTGGGC AGCATGGACA GTCCCCCACT CAGAAGTGCA AGAGTTCCAA AGAGCCTCTG 1380
GCCCAGGCCC CTCCCCACCA GGGCTTTGCA GATGTCCTTG AAAGACCCAC CCTAGAGCCC 1440
TTTGGAGTGC TGGCCCCTCC TGTGCCCTCT GCCCTGGTGG AAGCGGCAGC CACAAGTCCT 1500
CCTCAGGGAG CCCCAAGGGG GATTTTGTGG GACCGCTGCC CACAGATCCA GGTGTTGGAA 1560
GGGCAGCGGG TAAGGTTCCC AAGCCAGCCC CAACACCCTT CCCACTTGGC ACCCAGAGGG 1620
GGCTGTGGGT GGAGGCCTGA CTCCAGGCCT CTCCTGCCCA CACCCTCTGG GCTGAGTTCC 1680
TTCTTTCCCT TGGACGCCCA GTGCTGGCCT TGGAGGACGG TCAGCTGGAG GATGGCGGTG 1740
GGGGAGGCTG TCTTTGTACC ACTGCAGCAT CCCCCACTTC TCCACGGAAG CCCCATCCCA 1800
AAGCTGCTGC CTGGCCCCTT GCTGTAAAGT GTGAAGGGGG CGGCTGAGTT CTCTTAGGAC 1860
CCAGAGCCAG GGCCCTCAAC TTCCATCCTG CGGGAGGCCT TGGCCGGGCA CTGCCAGTGT 1920
CTTCCAGAGC CACACCAGG GACCACGGGA GGATCCTGAC CCCTGCAGGG CTCAGGGGTC 1980
AGCAGGGACC CACTGCCCCA TCTCCCTCTC CCCACCAAGA CAGCCCCAGA AGGAGCAGCC 2040
AGCTGGGATG GGAACCCAAG GCTGTCCACA TCTGGCTTTT GTGGGACTCA GAAAGGGAAG 2100
CAGAACTGAG GGCTGGGATA TTCTCATGG TGGCAGCGCT CATAGCGAAA GCCTACTGTA 2160
ATATGCACCC ATCTCATCCA CGTAGTAAAG TGAACCTAAA AATTCAATCA AATGAACAAT 2220
TAAATAAACA CCTGTGTGTT TAAGAAAAAA AAAAAAAAAA A 2261

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Ala Ser Thr Ile Ser Ala Tyr Lys Glu Lys Met Lys Glu Leu Ser
1 5 10 15
Val Leu Ser Leu Ile Cys Ser Cys Phe Tyr Thr Gln Pro His Pro Asn
20 25 30

Thr	Val	Tyr	Gln	Tyr	Gly	Asp	Met	Glu	Val	Lys	Gln	Leu	Asp	Lys	Arg			
	35						40					45						
Ala	Ser	Gly	Gln	Ser	Phe	Glu	Val	Ile	Leu	Lys	Ser	Pro	Ser	Asp	Leu			
	50					55					60							
Ser	Pro	Glu	Ser	Pro	Met	Leu	Ser	Ser	Pro	Pro	Lys	Lys	Lys	Asp	Thr			
65					70					75					80			
Ser	Leu	Glu	Glu	Leu	Gln	Lys	Arg	Leu	Glu	Ala	Ala	Glu	Glu	Arg	Arg			
				85					90					95				
Lys	Thr	Gln	Glu	Ala	Gln	Val	Leu	Lys	Gln	Leu	Ala	Glu	Arg	Arg	Glu			
		100						105					110					
His	Glu	Arg	Glu	Val	Leu	His	Lys	Ala	Leu	Glu	Glu	Asn	Asn	Asn	Phe			
		115					120					125						
Ser	Arg	Gln	Ala	Glu	Glu	Lys	Leu	Asn	Tyr	Lys	Met	Glu	Leu	Ser	Lys			
	130					135					140							
Glu	Ile	Arg	Glu	Ala	His	Leu	Ala	Ala	Leu	Arg	Glu	Arg	Leu	Arg	Glu			
145					150					155					160			
Lys	Glu	Leu	His	Ala	Ala	Glu	Val	Arg	Arg	Asn	Lys	Glu	Gln	Arg	Glu			
				165				170						175				
Glu	Met	Ser	Gly															
			180															

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGCCAAAGAG GCCTAGGAGC CTCGTGGCTG CGTCACCGCC GCCCCCCCAG ACAAGATGGA	60
CACCGCGGAG GAAGACATAT GTAGAGTGTG TCGGTCAGAA GGAACACCTG AGAAACCGCT	120
TTATCATCCT TGTGTATGTA CTGGCAGTAT TAAGTTTATC CATCAAGAAT GCTTAGTTCA	180
ATGGCTGAAA CACAGTCGAA AAGAATACTG TGAATTATGC AAGCACAGAT TTGCTTTTAC	240
ACCAATTTAT TCTCCAGATA TGCCTTCACG GCTTCCAATT CAAGACATAT TTGCTGGACT	300
GGTTACAAGT ATTGGCACTG CAATACGATA TTGGTTTCAT TATACACTTG TGGCCTTTGC	360
ATGGTTGGGA GTTGTTCCCTC TTACAGCATG CCGCATCTAC AAGTGCTTGT TTAGTGCTC	420
CCGTGAGCTC ACTACTGACG CTGCCCATTG GATATGCTGT CAACCGGAAA ATTTGTTGGC	480

AGATTGTTTG	CAGGGTTGTT	TTGTGGTGAC	GTGCACACTG	TGTGCATTCA	TCAGCCTGGT	540
GTGGTTGAGA	GAGCAGATAG	TCCATGGGGG	AGCACCAATT	TGGTTGGAGC	ATGCTGCCCC	600
ACCGTTCAAT	GCTGCGGGGC	ATCACCAAAA	TGAGGCTCCA	GCAGGAGGAA	ATGGTGCAGA	660
AAATGTTGCT	GCTGATCAGC	CTGCTAACCC	ACCAGCTGAG	AACGCAGTGG	TGGGGGAAAA	720
CCCTGATGCC	CAGGATGACC	AGGCAGAAGA	GGAGGAGGAG	GACAATGAGG	AGGAAGATGA	780
CGCTGGTGTG	GAGGATGGCG	GCAGATGCTA	ATAACGGAGC	CCAGGATGAC	ATGAATTGGA	840
ATGCTTTAGA	ATGGGACCGA	GCTGCTGAAG	AGCTTACATG	GGAAAGAATG	CTAGGACTTG	900
ATGGATCACT	AGTTTTTCTG	GAACATGTCT	TCTGGGTGGT	ATCTTTAAAT	ACACTGTTCA	960
TTCTTGTTTT	TGCATTTTGC	CCTTACCATA	TTGGTCATTT	CTCCCTTGTT	GTTTGGGAT	1020
TTGAAGAACA	CGTCCAAGCA	TCTCATTTTG	AAGGCCTAAT	CACAACCATA	GTTGGGTATA	1080
TACTTTTAGC	AATAACACTG	ATAATTTGTC	ATGGCTTGGC	AACTCTTG TG	AAATTTTCATA	1140
GATCTCGTCG	CTTACTGGGA	GTCTGCTATA	TTGTTGTTAA	GGTCTCTTTG	TTAGTGGTGG	1200
TAGAAATTGG	AGTATTCCCT	CTCATTTGTG	GTGGTGGCT	GGATATCTGT	TCCTTGAAAA	1260
TGTTTGATGC	TACTCTGAAA	GATCGAGAAC	TGAGCTTTCA	GTCGGCTCCA	GGTACTACCA	1320
TGTTTCTGCA	TTGGCTAGTG	GGAATGGTAT	ATGTCTTCTA	CTTTGCCCTCC	TTCATTCTAT	1380
TACTGAGAGA	GGTACTTCGA	CCTGGTGTCC	TGTGGTTTCT	AAGGAATTTG	AATGATCCAG	1440
ATTTCAATCC	AGTACAGGAA	ATGATCCATT	TGCCAATATA	TAGGCATCTC	CGAAGATTTA	1500
TTTTGTCA GT	GATTGTCTTT	GGCTCCATTG	TCCTCCTGAT	GCTTTGGCTT	CCTATACGTA	1560
TAATTAAGAG	TGTGCTGCCT	AATTTTCTTC	CATACAATGT	CATGCTCTAC	AGTGATGCTC	1620
CAGTGAGTGA	ACTGTCCCTC	GAGCTGCTTC	TGCTTCAGGT	TGTCTTGCCA	GCATTACTCG	1680
AACAGGGACA	CACGAGGCAG	TGGCTGAAGG	GGCTGGTGCG	AGCGTGGACT	GTGACCGCCG	1740
GATACTTGCT	GGATCTTCAT	TCTTATTTAT	TGGGAGACCA	GGAAGAAAAT	GAAAACAGTG	1800
CAAATCAACA	AGTTAACAAT	AATCAGCATG	CTCGAAATAA	CAACGCTATT	CCTGTGGTGG	1860
GAGAAGGCCT	TCATGCAGCC	CACCAAGCCA	TACTCCAGCA	GGGAGGGCCT	GTTGGCTTTC	1920
AGCCTTACCG	CCGACCTTTA	AATTTTCCAC	TCAGGATATT	TCTGTTGATT	GTCTTCATGT	1980
GTATAACATT	ACTGATTGCC	AGCCTCATCT	GCCTTACTTT	ACCAGTATTT	GCTGGCCGTT	2040
GGTTAATGTC	GTTTTGGACG	GGGACTGCCA	AAATCCATGA	GCTCTACACA	GCTGCTTG TG	2100
GTCTCTATGT	TTGCTGGCTA	ACCATAAGGG	CTGTGACGGT	GATGGTGGCA	TGGATGCCTC	2160
AGGGACGCAG	AGTGATCTTC	CAGAAGGTTA	AAGAGTGGTC	TCTCATGATC	ATGAAGACTT	2220

TGATAGTTGC GGTGCTGTTG GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC 2280
 TGGTCATTGT GGCTCCCCTG AGGGTTCCTT TGGATCAGAC TCCTCTTTTT TATCCATGGC 2340
 AGGACTGGGC ACTTGGAGTC CTGCATGCCA AAATCATTGC AGCTATAACA TTGATGGGTC 2400
 CTCAGTGGTG GTTGAAAAC TGAATTGAAC AGGTTTACGC AAATGGCATC CGGAACATTG 2460
 ACCTTCACTA TATTGTTCGT AAAGTGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC 2520
 TGTGTGTACC TTATGTCATA GCTTCTGGTG TTGTTCTTTT ACTAGGTGTT ACTGCGGAAA 2580
 TGCAAACTT AGTCCATCGG CGGATTTATC CATTTTTACT GATGGTCGTG GTATTGATGG 2640
 CAATTTTGTC CTTCCAAGTC CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA 2700
 AGTACCTTGK GGGTCAASGA CTCGGTGAAC TACGAACGGA AATCTGGGCA AACAAGGCTC 2760
 ATCTCCACCA CCTCCACAGT CATCCCAAGA ATAAAGTAGT TGTCTCAACA ACTTGACCTT 2820
 CCCCTTTACA TGTCCTTTTT TGTGGACTTC TCTCTTKGGA GATTTTTCCT AGTGATCTCT 2880
 CAGCGTKGTT TTTAAGTTAA AKGTATTKGA CTTGTGTTCT CAGCATTCAG AGAGCAGCGG 2940
 TGTAAGATTC TGCTGTTCTC CCTGGATCTT CTGACATKAC TGCTGTCTGA GATTGTGATA 3000
 TGKGTAAATA CAAGTTCCTT GATACCCTAA AACCTTGGAT TAAACAGAAT GTGCATKGTA 3060
 CATCTTTAAA CAAAATGKAT ATTAATTTAT TAAAAAAAAA AAAAAAAAAA 3109

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Gly	Glu	His	Gln	Phe	Gly	Trp	Ser	Met	Leu	Pro	His	Arg	Ser	Met
1				5				10						15	
Leu	Arg	Gly	Ile	Thr	Lys	Met	Arg	Leu	Gln	Gln	Glu	Glu	Met	Val	Gln
			20					25						30	
Lys	Met	Leu	Leu	Leu	Ile	Ser	Leu	Leu	Thr	His	Gln	Leu	Arg	Thr	Gln
			35					40						45	
Trp	Trp	Gly	Lys	Thr	Leu	Met	Pro	Arg	Met	Thr	Arg	Gln	Lys	Arg	Arg
			50					55						60	
Arg	Arg	Thr	Met	Arg	Arg	Lys	Met	Thr	Leu	Val	Trp	Arg	Met	Ala	Ala
			65					70						75	
															80

Asp	Ala	Asn	Asn	Gly	Ala	Gln	Asp	Asp	Met	Asn	Trp	Asn	Ala	Leu	Glu	85	90	95
Trp	Asp	Arg	Ala	Ala	Glu	Glu	Leu	Thr	Trp	Glu	Arg	Met	Leu	Gly	Leu	100	105	110
Asp	Gly	Ser	Leu	Val	Phe	Leu	Glu	His	Val	Phe	Trp	Val	Val	Ser	Leu	115	120	125
Asn	Thr	Leu	Phe	Ile	Leu	Val	Phe	Ala	Phe	Cys	Pro	Tyr	His	Ile	Gly	130	135	140
His	Phe	Ser	Leu	Val	Gly	Leu	Gly	Phe	Glu	Glu	His	Val	Gln	Ala	Ser	145	150	155
His	Phe	Glu	Gly	Leu	Ile	Thr	Thr	Ile	Val	Gly	Tyr	Ile	Leu	Leu	Ala	165	170	175
Ile	Thr	Leu	Ile	Ile	Cys	His	Gly	Leu	Ala	Thr	Leu	Val	Lys	Phe	His	180	185	190
Arg	Ser	Arg	Arg	Leu	Leu	Gly	Val	Cys	Tyr	Ile	Val	Val	Lys	Val	Ser	195	200	205
Leu	Leu	Val	Val	Val	Glu	Ile	Gly	Val	Phe	Pro	Leu	Ile	Cys	Gly	Trp	210	215	220
Trp	Leu	Asp	Ile	Cys	Ser	Leu	Glu	Met	Phe	Asp	Ala	Thr	Leu	Lys	Asp	225	230	235
Arg	Glu	Leu	Ser	Phe	Gln	Ser	Ala	Pro	Gly	Thr	Thr	Met	Phe	Leu	His	245	250	255
Trp	Leu	Val	Gly	Met	Val	Tyr	Val	Phe	Tyr	Phe	Ala	Ser	Phe	Ile	Leu	260	265	270
Leu	Leu	Arg	Glu	Val	Leu	Arg	Pro	Gly	Val	Leu	Trp	Phe	Leu	Arg	Asn	275	280	285
Leu	Asn	Asp	Pro	Asp	Phe	Asn	Pro	Val	Gln	Glu	Met	Ile	His	Leu	Pro	290	295	300
Ile	Tyr	Arg	His	Leu	Arg	Arg	Phe	Ile	Leu	Ser	Val	Ile	Val	Phe	Gly	305	310	315
Ser	Ile	Val	Leu	Leu	Met	Leu	Trp	Leu	Pro	Ile	Arg	Ile	Ile	Lys	Ser	325	330	335
Val	Leu	Pro	Asn	Phe	Leu	Pro	Tyr	Asn	Val	Met	Leu	Tyr	Ser	Asp	Ala	340	345	350
Pro	Val	Ser	Glu	Leu	Ser	Leu	Glu	Leu	Leu	Leu	Gln	Val	Val	Leu		355	360	365
Pro	Ala	Leu	Leu	Glu	Gln	Gly	His	Thr	Arg	Gln	Trp	Leu	Lys	Gly	Leu	370	375	380

Val	Arg	Ala	Trp	Thr	Val	Thr	Ala	Gly	Tyr	Leu	Leu	Asp	Leu	His	Ser	385	390	395	400
Tyr	Leu	Leu	Gly	Asp	Gln	Glu	Glu	Asn	Glu	Asn	Ser	Ala	Asn	Gln	Gln	405	410	415	
Val	Asn	Asn	Asn	Gln	His	Ala	Arg	Asn	Asn	Asn	Ala	Ile	Pro	Val	Val	420	425	430	
Gly	Glu	Gly	Leu	His	Ala	Ala	His	Gln	Ala	Ile	Leu	Gln	Gln	Gly	Gly	435	440	445	
Pro	Val	Gly	Phe	Gln	Pro	Tyr	Arg	Arg	Pro	Leu	Asn	Phe	Pro	Leu	Arg	450	455	460	
Ile	Phe	Leu	Leu	Ile	Val	Phe	Met	Cys	Ile	Thr	Leu	Leu	Ile	Ala	Ser	465	470	475	480
Leu	Ile	Cys	Leu	Thr	Leu	Pro	Val	Phe	Ala	Gly	Arg	Trp	Leu	Met	Ser	485	490	495	
Phe	Trp	Thr	Gly	Thr	Ala	Lys	Ile	His	Glu	Leu	Tyr	Thr	Ala	Ala	Cys	500	505	510	
Gly	Leu	Tyr	Val	Cys	Trp	Leu	Thr	Ile	Arg	Ala	Val	Thr	Val	Met	Val	515	520	525	
Ala	Trp	Met	Pro	Gln	Gly	Arg	Arg	Val	Ile	Phe	Gln	Lys	Val	Lys	Glu	530	535	540	
Trp	Ser	Leu	Met	Ile	Met	Lys	Thr	Leu	Ile	Val	Ala	Val	Leu	Leu	Ala	545	550	555	560
Gly	Val	Val	Pro	Leu	Leu	Leu	Gly	Leu	Leu	Phe	Glu	Leu	Val	Ile	Val	565	570	575	
Ala	Pro	Leu	Arg	Val	Pro	Leu	Asp	Gln	Thr	Pro	Leu	Phe	Tyr	Pro	Trp	580	585	590	
Gln	Asp	Trp	Ala	Leu	Gly	Val	Leu	His	Ala	Lys	Ile	Ile	Ala	Ala	Ile	595	600	605	
Thr	Leu	Met	Gly	Pro	Gln	Trp	Trp	Leu	Lys	Thr	Val	Ile	Glu	Gln	Val	610	615	620	
Tyr	Ala	Asn	Gly	Ile	Arg	Asn	Ile	Asp	Leu	His	Tyr	Ile	Val	Arg	Lys	625	630	635	640
Leu	Ala	Ala	Pro	Val	Ile	Ser	Val	Leu	Leu	Leu	Ser	Leu	Cys	Val	Pro	645	650	655	
Tyr	Val	Ile	Ala	Ser	Gly	Val	Val	Pro	Leu	Leu	Gly	Val	Thr	Ala	Glu	660	665	670	
Met	Gln	Asn	Leu	Val	His	Arg	Arg	Ile	Tyr	Pro	Phe	Leu	Leu	Met	Val	675	680	685	

Val	Val	Leu	Met	Ala	Ile	Leu	Ser	Phe	Gln	Val	Arg	Gln	Phe	Lys	Arg
690						695					700				
Leu	Tyr	Glu	His	Ile	Lys	Asn	Asp	Lys	Tyr	Leu	Xaa	Gly	Gln	Xaa	Leu
705					710					715					720
Gly	Glu	Leu	Arg	Thr	Glu	Ile	Trp	Ala	Asn	Lys	Ala	His	Leu	His	His
				725					730					735	
Leu	His	Ser	His	Pro	Lys	Asn	Lys	Val	Val	Val	Ser	Thr	Thr		
				740				745					750		

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TNTTTGAAGT TTCTCCCTCT CATTCTGAG

29

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GNTTCTCCAC GTAGTTGGTT TTCCTCAGT

29

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CNACATGACG TGAGCTGGTG ATCCATGAA

29

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ANTTGGGCTC TGCCGTCCAG AAAGGTTTG

29

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GNAGCTACGC GGACTTGCG AGGTTTTAT

29

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TNGGTGAGAG AATAGAGACT GGCTGGGAA

29

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ANGAGCCGAC CAGACGTGCA AGATGCATA

29

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ANCTGACCAG GACTCTCCTT CCACAGAGG

29

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TNTAGGCGGA AATGGTGCTG GCCATGGTG

29

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:
ANATATCCAG CCACCAACCA CAAATGAGA

29

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GCTAATTTGA GAAGAAAACA AGTAGGATTT TTGTTTTGTT TTGCATTTTG CAATATGGAG 60
GAGAAATGAT TAGACCTTAG GAAGTGCCAG TGGGTTGGTC CTTTCATGAA CATGCCATCA 120
GTAAAAGCCC TGGAACAAG GTCATACCAG AGATTCATTG TGCCTTGTC CAACTGCAAA 180
CAATATCTGA GTGGAATATT CAAAACTTG CTTAGAAAAGA AACTCTAGG ACAGATGGCT 240
CCACTGAAGT TATTCCAAAT ATTTAATAAA TAAAGCATAC CAGGCTTTTA TAACTCTTC 300
TAGAAGAAAA AAGTTGGAAC TTTTCCAATT CAGTTTTTCA GGCCAGTGCA ACCTTGATAC 360
CAAAACCAAT AAAACAAACA AACAAACAAA AACATAAAG CTATAGACCA AAGTCTCATA 420
GATTTAGATG CAAAATCCTA AAATTGAAAA AAAAAGTCTA GTCATATCCA TAACTGTAT 480
CATCACCAAG AGATGTTTAT TAGGGCAATC AAAAGATGAT TTATTATTTT TTAAAAAATC 540
AATGTGGCCT TCCCTTCCTC TTTCTTTTGA TTCCCTCTT TGAGTTTTTA TGTGTCTCTT 600
TTGCCTTCCC TTCCAGAGT GGAGGAGTTA GACCTGCATT GTGGGATGAG AGGAGTTGTG 660
GCTATGTGTC TGCTGGCACC AAGAGGGCTG AGGGTGAGGT GTGGAAGGGA CAGGGGGAGG 720
AGATGGGCAG CATTGTTAAG AGATTGGTAC CACTGAGCAA ATATGTTGAG AATGATGATG 780

GCAAGGTTTC TCCCTGTTAG AGAAGGTATT TGTAGAAATA GGAATGAGGA GAGCTAGAAA 840
 ACCTGGAGTG TGGGATTAGA ATAGAACTCA TATCTTTTAA ATACATAGGA ACAATAGAGA 900
 AATTGTTGGG TGTGCCATA TACATATATT TTGTGATTCA TTCTACCGAG AGGACATAAA 960
 TGCAGTCACA GCTCAGTAAC AGTAAACACA CCAACTGCCA AGTTATTATT TCCTAAATAC 1020
 TATCCACAAA AAAGGGGACC AGGGATGATT CCTAGTCGGA GATTGGGAGA AAAAGAAGAT 1080
 GAGCCTGAAT CATTTTCATGT ACCTAACAGA AAGAAAATAC TCTGGCTGGG CTCAGWGGCT 1140
 CATGTTTGTA ATTCTAGCAT GTTAGGAGGT CGAGGTGGGT GTGTTGCTTG AGCCCAGGAG 1200
 TTTGAGACCA GCCCAGGCAA CATGGCAAAA CTGTCTCTAC AAAAAATATA AAAGTTAGCC 1260
 AGGCGTGGTG GCATGCGCCT GTCGTCCGAG ATACTCGGGA GGCAGAGAGG TGGGAGGATC 1320
 ACTTGAGCCT GGGAGATTGA GACTGCATCG AGCTGTGGTC ATGCCACTGC ACTCCAGCCT 1380
 GGAGGACAGA GTGAGACCCT GTCTCAGGAA AAAAAAAAAA AAAAA 1425

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met	Ile	Tyr	Tyr	Phe	Leu	Lys	Asn	Gln	Cys	Gly	Leu	Pro	Phe	Leu	Phe
1				5					10					15	
Leu	Leu	Ile	Pro	Leu	Phe	Glu	Phe	Leu	Cys	Val	Ser	Phe	Ala	Phe	Pro
			20					25					30		
Ser	Gln	Ser	Gly	Gly	Val	Arg	Pro	Ala	Leu	Trp	Asp	Glu	Arg	Ser	Cys
		35					40					45			
Gly	Tyr	Val	Ser	Ala	Gly	Thr	Lys	Arg	Ala	Glu	Gly	Glu	Val	Trp	Lys
	50					55					60				
Gly	Gln	Gly	Glu	Glu	Met	Gly	Ser	Ile	Val	Lys	Arg	Leu	Val	Pro	Leu
65					70					75				80	
Ser	Lys	Tyr	Val	Glu	Asn	Asp	Asp	Gly	Lys	Val	Ser	Pro	Cys		
				85					90						

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CGCACCCAGC	CGCGCCGGCG	AGGACATGGG	CAGCCGCGGC	GCGCCCACCC	CCCGCGCCGA	60
TGTGAATTAT	TAAAAAGAAA	ATGGCCCAAC	GGAGCACTGT	ATTTCTTCT	CGTGTCACCA	120
AGGAAAGGTA	TAATATATGG	AAAATATGCA	TCTAAGGCGA	GTGAGAACCA	TGCCCCGACA	180
CAGCCAGTCC	CTGACCATGG	CACCATACTC	ATCTGTAAGC	CTCGTGGAGC	AGCTGGAAGA	240
CAGGATCCTC	TGCCATGAGA	AAACCACCGC	CGCCCTCGTA	GAGCACGCCT	TTCGGATTAA	300
AGATGACATT	GTCAACAGTT	TGCAGAAAAT	GCAAAACAAA	GGGGGAGGTG	ACCGCTTGGC	360
CAGGCTTTTC	TTGGAGGAGC	ATATCAGAAA	CATAACTGCC	ATAGTGAAGC	AACTTAATCG	420
GGATATCGAG	GTACTIONCAGG	AGCAGATTCG	TGCTCGGGAC	AACATTAGCT	ATGGAACATA	480
TTCTGCCTTA	AAGACCCTGG	AGATGCGCCA	GCTCTCCGGT	TTGGGAGATC	TTGAGGAAG	540
AGTGGCAAGA	TGTGATGCCA	GCATAGCTAG	ACTTCTGCA	GAGCACAAAA	CGACCTATGA	600
GGGGCTCCAG	CACTTGAACA	AAGAACAGCA	GGCTGCCAAA	CTTATCTTGG	AAACGAAAAAT	660
CAAAGATGCA	GAGGGACAGA	TTTCTCAGCT	TTTGAACAGA	GTGGACTTGT	CAATATCAGA	720
GCAGAGCACC	AAACTGAAGA	TGTCTCACAG	AGACAGTAAC	CACCAGCTTC	AGCTTTTGGA	780
CACTAAATTT	AAAGGTACAG	TTGAGGAACT	CAGTAACCAG	ATATTATCTG	CACGGAGTTG	840
GTTGCAACAG	GAACAAGAAC	GGATAGAAAA	AGAGCTTTTA	CAGAAAAATTG	ATCAGCTTTC	900
CTTGATTGTT	AAGGAAAACA	GTGGAGCCAG	TGAAAGGGAT	ATGGAGAAGA	AGCTCAGCCA	960
GATGTCAGCC	AGGCTTGACA	AAATAGAAGA	GGGTCAAAAG	AAGACTTTTG	ATGGTCAGAG	1020
AACAAGGCAA	GAAGAGGAGA	AGATGCACGG	GCGAATCACC	AAGCTGGAGT	TACAGATGAA	1080
CCAGAACATC	AAGGAAATGA	AAGCAGAAGT	TAATGCTGGG	TTTACAGCCG	TCTATGAAAG	1140
CATAGGATCC	CTCAGGCAAG	TTCTCGAGGC	CAAGATGAAG	CTGGACAGGG	ACCAGCTACA	1200
GAAGCAAATC	CAGCTGATGC	AGAAGCCAGA	GACCCCATG	TGAAGGGAGC	TGGGACAAGG	1260
TCCTAAAAGA	CAGTTTTGCC	AGTGGGGCTA	GGAGCCGGAT	ACCTCTGTAG	CCAGGCCATC	1320
GCTGCATTCA	GGATTGTTCC	ATCCATGGCG	TGCATGTGCC	AAGAAATGTG	TTTTTATGGG	1380
TCTAAATGTT	TACCTTGAGT	CTTGAAAATA	CTCTTTTGTT	AAAAGTATGA	AATACAGTTT	1440

TTACCAGTTT	ATTTCACTTC	TCTAAATTCA	ATGGAAATCC	CCCGCCCTGG	ATTTTGAAAG	1500
GCTTTTATCT	TCTTCATTTT	ACGAATGGAA	AGACGACAAT	TTTTCTTCAA	TGCTTGATGC	1560
ACTAATGAAG	ACTGTTTACT	ATTTTGAAAA	ATGTCATGGG	GATTTTTTTT	TAATTAAGAA	1620
ACTAATGAAT	CATCACAGGA	ATGTGTTGCT	CCTCACCCCTA	AATTAAGAGA	ATGTCCCAGT	1680
AGATTAGACT	TCAACCTTTG	AGTCCAATTT	GGATTTTATT	ATCGTTGTCT	ATGCACTTCT	1740
TATATTGGTT	ATCTTCTTGT	AAATCTTCTG	TCTTTTGTAA	GGGGAAAGGA	TTTAACATTT	1800
AGAATAAACC	CCACCATTTA	TGTAATGGAA	ATAGTTTAAA	AATTGCTAAC	TGCCATGTGG	1860
ATTGCAAAT	AAATGGAAAC	TTATTTAGAT	AACGTAAGGC	TCAATATCTG	CGTTGACCAC	1920
CTAGATATTA	CAGGTTTTTA	TATTTAAAAC	TATTTTGTAA	TTATCCACAA	CCTGTATAGT	1980
GATAGCCATA	TATTTAATAA	TGGAATGGTG	GTTAACAGTC	TATTTACTGC	ACAATTAATT	2040
GTTCACTAAT	CAAATAGAAT	GTGGTAATTT	TTCAGACTTT	ATGATCTGTT	TCCAAAATTG	2100
GCACAAAGTG	CTAGGGTTTA	TATACACTTA	TCGTAACTGT	ATTTTGTGTC	CTTGGTTTTA	2160
TCATGTCAAT	GCACTGTACT	CTGTAAAAGT	TTTGCAGACA	AAATAGAAAG	TATGATAATC	2220
CGTCAGAAGT	ATGATGTAAA	ACTGGAATCC	TCTGTATTTT	TTAAATGTTC	TAAAAATTTT	2280
ATCGCTGTTA	AGGTATTAAT	CATTCAGTAT	TACTAATGGA	ATAGAAATTC	ATACTTTTGT	2340
ATGGACAACA	AATTGATATT	GCATTTATAG	CACTGTAAGA	AACTTTCATC	TTGAGCAACT	2400
TTGTAGATGA	TGGGTGTTTT	ATTTTCAATC	GCCATATTTG	ATCAGTCATT	GAAAATTGGC	2460
CCCAGTGCTG	TTTGTTTCATC	TCTGTATGTA	AAAACTGACA	GTGAGACACA	ACTTTCTGAA	2520
CTGTGAGGGT	GTCCCAGGAA	AAAGAAAAAC	AGGAATACTT	TAACAATTAA	AAAGAAAAAA	2580
ATGTTTTTTG	TTTGCCAAGG	ACTCAGGAAA	ATAAAAAGCA	TTTTCTATTT	TTAGGACAAA	2640
TCACAAATGA	AGTGTCTAAC	TGGCTATTAC	TGTTTACCCA	TATAAAATAT	GCTGCTAAAG	2700
TACATATTTT	GCTGTCAATG	GCTTGACAAT	TTTTTTTTTC	AAATTGAC	ATGAGAGGTT	2760
ATATAGGGAC	TATATTATCC	AACACATATT	TTCTTATTTT	GCCACAAATT	TCCACTTAAC	2820
AAATAAAAAA	AGGCGAATGC	TGTTTTGCAA	AAAAAAAAAA			2859

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Glu	Asn	Met	His	Leu	Arg	Arg	Val	Arg	Thr	Met	Pro	Arg	His	Ser		
				5					10					15			
Gln	Ser	Leu	Thr	Met	Ala	Pro	Tyr	Ser	Ser	Val	Ser	Leu	Val	Glu	Gln		
				20					25					30			
Leu	Glu	Asp	Arg	Ile	Leu	Cys	His	Glu	Lys	Thr	Thr	Ala	Ala	Leu	Val		
				35					40					45			
Glu	His	Ala	Phe	Arg	Ile	Lys	Asp	Asp	Ile	Val	Asn	Ser	Leu	Gln	Lys		
				50					55					60			
Met	Gln	Asn	Lys	Gly	Gly	Gly	Asp	Arg	Leu	Ala	Arg	Leu	Phe	Leu	Glu		
65					70					75					80		
Glu	His	Ile	Arg	Asn	Ile	Thr	Ala	Ile	Val	Lys	Gln	Leu	Asn	Arg	Asp		
				85					90					95			
Ile	Glu	Val	Leu	Gln	Glu	Gln	Ile	Arg	Ala	Arg	Asp	Asn	Ile	Ser	Tyr		
				100					105					110			
Gly	Thr	Asn	Ser	Ala	Leu	Lys	Thr	Leu	Glu	Met	Arg	Gln	Leu	Ser	Gly		
				115					120					125			
Leu	Gly	Asp	Leu	Arg	Gly	Arg	Val	Ala	Arg	Cys	Asp	Ala	Ser	Ile	Ala		
				130					135					140			
Arg	Leu	Ser	Ala	Glu	His	Lys	Thr	Thr	Tyr	Glu	Gly	Leu	Gln	His	Leu		
145					150					155					160		
Asn	Lys	Glu	Gln	Gln	Ala	Ala	Lys	Leu	Ile	Leu	Glu	Thr	Lys	Ile	Lys		
				165					170					175			
Asp	Ala	Glu	Gly	Gln	Ile	Ser	Gln	Leu	Leu	Asn	Arg	Val	Asp	Leu	Ser		
				180					185					190			
Ile	Ser	Glu	Gln	Ser	Thr	Lys	Leu	Lys	Met	Ser	His	Arg	Asp	Ser	Asn		
				195					200					205			
His	Gln	Leu	Gln	Leu	Leu	Asp	Thr	Lys	Phe	Lys	Gly	Thr	Val	Glu	Glu		
				210					215					220			
Leu	Ser	Asn	Gln	Ile	Leu	Ser	Ala	Arg	Ser	Trp	Leu	Gln	Gln	Glu	Gln		
225					230					235					240		
Glu	Arg	Ile	Glu	Lys	Glu	Leu	Leu	Gln	Lys	Ile	Asp	Gln	Leu	Ser	Leu		
				245					250					255			
Ile	Val	Lys	Glu	Asn	Ser	Gly	Ala	Ser	Glu	Arg	Asp	Met	Glu	Lys	Lys		
				260					265					270			

Leu Ser Gln Met Ser Ala Arg Leu Asp Lys Ile Glu Glu Gly Gln Lys
 275 280 285
 Lys Thr Phe Asp Gly Gln Arg Thr Arg Gln Glu Glu Glu Lys Met His
 290 295 300
 Gly Arg Ile Thr Lys Leu Glu Leu Gln Met Asn Gln Asn Ile Lys Glu
 305 310 315 320
 Met Lys Ala Glu Val Asn Ala Gly Phe Thr Ala Val Tyr Glu Ser Ile
 325 330 335
 Gly Ser Leu Arg Gln Val Leu Glu Ala Lys Met Lys Leu Asp Arg Asp
 340 345 350
 Gln Leu Gln Lys Gln Ile Gln Leu Met Gln Lys Pro Glu Thr Pro Met
 355 360 365

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 933 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGCTTCGGAG ACCGTAAGGA TATTGATGAC CATGAGATCC CTGCTCAGAA CCCCCTTCCT	60
GTGTGGCCTG CTCTGGGCCT TTTGTGCCCC AGGCGCCAGG GCTGAGGAGC CTGCAGCCAG	120
CTTCTCCCAA CCCGGCAGCA TGGGCCTGGA TAAGAACACA GTGCACGACC AAGAGTACGT	180
ATTCAGCCCG GGCTGTGGTC CAGTGGCCTC CCCATCATCT GCAGCTGAGC CAGCGGCAAG	240
GGCATGCTCA GTCCTCCTTT CCTTCTTCCT GTTTCTATGG CTCCTTGACA TTCTTCAAGG	300
ATGATTCTTA TTCCTTATTG CCACCTATAA GTCAGGTATT CTTTTTTCAT CATTGTATCA	360
CAGGTGGAAG ATCTTTAGGC CCAAATGGGG CACATTACTT GTCTGAATCC GGTCTCTCCT	420
TTTTTTCACC ACAGACAGAC ACACACACAT ACAAATAGAC ACACAGGTAC ACATACACAG	480
TCATAGTAGC AGAATCCAGA AAATAGCTAA GGTTCCTTGA CTATAACAAG ACCTTTTTTA	540
AATCAACACA TTCAAACATT GAATCATTTG TTGCAGCTTT TGTCTTGGGC CAGTTAGCCT	600
CACGCATTAT ACTCGGTTAT CCTTTGTTTT TAAGGCTGGG TGCAGTGGCT CACACCTGTA	660
ATCCCAGTGC TTTGGGAGGC TGAGGCAGGT GGATTACTTG AGCCCAGGAA TTCGAGACCA	720

GCCTAGGCAA TATAGGGAAA ACCTGTCTCT AYTAATAAAT TGCAATAAAT TAGCTGGATG 780
 TGGCAGTACA TGCCTATGGT CCCAGCTACT TGGGGGGCTG AAGTGGGAGA ATCAAMTGAG 840
 CTTGGGAAGT TGAGGCTACA ATGAGCCAAG ATCACGCTCC TGCACTCCAG CCTGGGTGGC 900
 AGAGTGAGAC CCTGTCTCAA AAAAAAAAAA AAA 933

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met	Thr	Met	Arg	Ser	Leu	Leu	Arg	Thr	Pro	Phe	Leu	Cys	Gly	Leu	Leu
1				5					10					15	
Trp	Ala	Phe	Cys	Ala	Pro	Gly	Ala	Arg	Ala	Glu	Glu	Pro	Ala	Ala	Ser
			20					25					30		
Phe	Ser	Gln	Pro	Gly	Ser	Met	Gly	Leu	Asp	Lys	Asn	Thr	Val	His	Asp
		35					40					45			
Gln	Glu	Tyr	Val	Phe	Ser	Pro	Gly	Cys	Gly	Pro	Val	Ala	Ser	Pro	Ser
		50				55					60				
Ser	Ala	Ala	Glu	Pro	Ala	Ala	Arg	Ala	Cys	Ser	Val	Leu	Leu	Ser	Phe
65					70					75				80	
Phe	Leu	Phe	Leu	Trp	Leu	Leu	Asp	Ile	Leu	Gln	Gly				
			85						90						

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2956 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGTGTGTGGT	GGTTTAAGAA	TGTATATCAT	AGGGTCAGGT	GGCCTGGGTT	CATTCCCCAG	60
CTACGTAACC	TTTCTATGCC	TGAGTTTCCT	CATCTATAAA	ACAAGGATAA	TAATAGTGTG	120
TACTTCTTAG	GATTGTTTTG	GAGACTCATA	AATGAGAAAT	ACGTGAAAAA	CTCCCTCAAG	180
GCAGTGCTTG	ACACATAATG	AGCACTCAGT	TATCATGGTC	ATCATGGTCA	TCATCACTGC	240
TACCACCACT	GCTGCTGCTA	TTACCACTCT	ACCTCTTCCC	CCTGAAACTC	TAATCACTTA	300
CCCTAGAAAC	AGTTAAATTA	CAC TTCAGTG	GGAAGGATCT	CAGATTTCTT	AATGGCACCT	360
GCATTTATAT	AATGTTGATA	TTGCACGTTT	CTAGAAAACA	TATCAAGAAG	AAACCAAAAT	420
GTGTTTCTGT	ACTTTGTAAA	CCTGTACAAT	AGTTAGAGAT	TAGAGGACCT	TTATAATCTA	480
CTACTAATTA	CTGTGAAAGT	AAACATTGTT	TAATATACCA	GTTCTTAAAG	AAATATTTTG	540
TCTAGTCATT	AATATTTCTAG	TTCATCTCAA	AGCTTCCATT	TGACAATTTA	AAATTACTTA	600
AATTTTAATA	TTAAAGGAAA	CAGTTTTTCCT	GATTCTCATG	AAAGTTCCTA	TTTGCACTGA	660
AGATGACTAA	ACCTTTTAGT	CATAGTTTTA	GAAGAATTGG	CTTTTTTATA	GCCATTTTAT	720
TTACATATGG	GTACTGCATA	GCAAAGGCAG	CAGATTAGCC	CTGTTTGTTT	TGCAGGGATG	780
AAAGGTAGCA	TTCCCAGAGA	TTAAGTTGTT	CTTGCTATTC	CCATTCTCTG	CTACATTTGC	840
CTACATTCTT	TGGTCCTTTC	TATTATTTGT	TTCTTTGGTG	GAATCCCCTT	GTTGCTTATG	900
GCTGGATATT	GTTATTCAGC	AGATGAATCA	CAAGTTTAGC	CTGAGGGCCC	TAAAGCATCA	960
GAAATAAATT	AGAGCCGAGC	AAAGTTTAAC	TTCTCTGGAA	CTTGCACCTT	TAGTTTCCAT	1020
GTATTTCTGG	AACCAAGATA	TTTCAAAGGC	TTACTTTATT	TCAGACACCT	ATTATCTTCA	1080
AGTCACAGAT	AACTATTGAT	TCTGTAAAGT	GTTTCAAAGA	TTTTTGTTCA	CTAGACATTT	1140
TTAAATTTGT	TCAACTCCTC	CTCATCATTT	TAGAAATTAT	TTCTGTTAGG	TAAAATTAAA	1200
ACTAACAATG	TATTTTAGTT	TATTTTTCTA	ATGATAACCAG	TCACCTTTCG	GGGCTAACTA	1260
AACATTTTGT	GCAGCATTCT	CTTAGTTTAC	ATCCTCCTTT	CTTTCAGTCT	TCCTGTTTAT	1320
TAAGGCTGTC	CTGTAGCAAA	CAAAAGAGTG	ACTCATGTTA	AAAGTATTTT	AACTGCTCTA	1380
ATATATCTGA	GGAAGAATAA	CTTTCCTAAAT	TAAAGTAATG	TATTTTATTA	AATATTAAAA	1440
TGCATTTTTT	GGCTATTCAT	TTCTGTATGT	AAAAGAAAAG	TTAACTTTAT	GGTGTTATGC	1500
AAAATATGCT	AAATTTAGAT	TTTAGAGCAA	TATATAGGGA	GATATGTCAC	AAATTTCTAC	1560
ATTTTGGTTA	AATTATTAGT	ATTTTTTTTAT	ATTCAAATGT	GCCTTGATAT	TTAAATAATA	1620
TACTGAATGC	AGAATTTATG	TTATGTGAAC	CATTATGGAA	AATGTTAATG	TTAACAAAAT	1680
GAGGTGTATT	GACTTTTCAA	CAATGTAAAT	TAAAGATGGT	ACATCTACTG	TTTAAGGGCA	1740

GAGGAATTAA AAGAGTATAG ATACTGAAAT GTATCACTTA CTAGTAGTGT GGCTATAATC	1800
AAATTAATTA ATCTCTCTCT AGGCCTTAGC TTCCTCATCT TAGTTTGTTT AGGCTACTGT	1860
AACAAAATAA CATAGATTAT GTACTTTTAA ATGACAGAAG TTTATTCGGC ATGGTTTGGG	1920
AGACTAGGAA GTCTAAGATT AAAGAACCAG CAAATTTGGT GTCTGATGAG GACCCATTCC	1980
TTTGTTTACA GATGATGCCT TCTCATTGTG TTTTCAAATG TTAGAAGGAG CTAGCTAGCT	2040
TTCTGGGGTC TCTTTTGTAA AGGCACTAAT CCCAGTCATT AGGGCAAATT GGCTCCTACA	2100
GGCCCCACCT ATCTCCTAAT ACCATCACCT TGAGGATTAA GATTTCTACA TATGAATGAA	2160
GCAGGTGTTG TAGAAGGTCA GTCAGTTAGA CCATAGCACC ATCTGTAAAA TTGAATAGTA	2220
ATTTACTGCC TCATTGGATG TCAGGATTAA AGGAGATAAG ATTTTATTAG TTACTAGTTA	2280
CCATAGTGGT TTTTTTTTTT CACTATAATG TTCGTTTTTT TGTTCATGC TTGTACCTTC	2340
AACATTTTCT TCCATTTGAA TACTTCTTTT GTCTCCTGTA GGCCTGTCTG TCCACTTAGG	2400
TGTAAGATGT GTTTTTGTGT CAGGAATGAT GGTGCAATGC TAATGTTCCA TTGCCCTATT	2460
TGGCAATACT CTGATCATT ACTATAAAGA ATAACACCAG TGTTAACTAA CTCTCCTTGC	2520
CTGACAGTAG TGCTGCCACT ATTCCTTGTT TCTGTGGTAA TAGATGAGGT TTGTATGGTC	2580
CTGTTATTCC AGCCTCCAGA CACCATTTCCA GATCAACTGG TGCCYTCWAC GCCCCCGAAG	2640
TGTATGGGGC CTCAGGTGAA GGATGAGWAC ATTTTCACTA TCATCTGGCA TTCATCTCAG	2700
ATTTTATCCT TTTCAGTTTC CATTAAATAA TATTCATGTT TTAAAATTGA TTTTTTATTA	2760
TTTAAATTTA ATTTGTTGGA GAATAAACTT TTTTTTTTCT TTTCTCCCAA GTAACGTTTT	2820
CCCCTTTAGC AACTGTATTG AGCATTTTTC TCACTGGTAT ATGGACATTT TTTTGTATAA	2880
CCTGTTGTGT CATTTTAAAA TATAGAATTG TTTTATGTT CTCATCTTTG TATATATGTT	2940
TAAAAAAAAA AAAAAA	2956

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Thr Lys Pro Phe Ser His Ser Phe Arg Arg Ile Gly Phe Phe Ile
 1 5 10 15

Ala Ile Leu Phe Thr Tyr Gly Tyr Cys Ile Ala Lys Ala Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AATCGGGAAA AAAAGCCATG TATTCTTTTCG TTTCTCTCTA AAAGAAGAAA AATATAATTT	60
AAAAATACAT TGC GTATTTT CTAAACAAT AAATTTATAG TGTTAATATT CATAGGGTCA	120
ATCAAAATGA AGCTTCTCCT TTGGGCCTGC ATTGTATGTG TTGCTTTTGC AAGGAAGAGA	180
CGGTTCCCCCT TCATTGGTGA GGATGACAAT GACGATGGTC ACCCACTTCA TCCATCTCTG	240
AATATTCCTT ATGGCATA CG GAATTTACCA CCTCCTCTTT ATTATCGCCC AGTGAATACA	300
GTCCCCAGTT ACCCTGGGAA TACTTACACT GACACAGGGT TACCTTCGTA TCCCTGGATT	360
CTAACTTCTC CTGGATTCCC CTATGTCTAT CACATCCGTG GTTTTCCCTT AGCTACTCAG	420
TTGAATGTTT CTCCTCTCCC TCCTAGGGGT TTCCCGTTTG TCCCTCCTTC AAGGTTTTTTT	480
TCAGCAGCTG CAGCACCCGC TGCCCCACCT ATTGCAGCTG AGCCTGCTGC AGCTGCACCT	540
CTTACATCCA CACCTGTAGC ATCTGAGCCT GCTGCAGGGG CCCCTGTTGC AGCTGAGCCT	600
GCTGCAGAGG CACCTGTTGG AGCTGAGCCT GCTGCAGAGG CACCTGTTGC AGCTGAGCCT	660
GCTGCAGAGG CACCTGTTGG AGTGGAGCCA GCTGCAGAGG AACCTTCACC AGCTGAGCCT	720
GCTACAGCCA AGCCTGCTGC CCCAGAACCT CACCCTTCTC CCTCTCTTGA ACAGGCAAAT	780
CAGTGAAATT CTCTAGAAGA GTACCATGGG TTCATTTCTA TACTGATGCA GAAATAAGTG	840
AAATCTACAA AAGTTTTCTT TCTTTTCCAA AGACTATTTT ATTCTGTAGT ATTCAGAGTA	900
TTCATCTCAC TACATAGATT TGTTTGTGGT AGTTATTTCC TTGGACTTAA TTTATATTGA	960
AAAAACATTG ATAATTAAAT AAATAAAATA GATAATTTAG ACCAATGGTG ATAAGGTCTG	1020
GATGAAAACT ACGCTATGGA GGACTGAAAT GGCAATCATT CAGCCTAGCC TGGAGTCTGA	1080

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TTATACAGCT ACTATAGGAT GATGTTAGTA TTGGTTTTGA GTGCAATAGG TTTTTCCTA      1140
AACAAACATA TTTTGTAGTC AATGAACTTT TTGTCACAAA ACAGTAAAAC ATCTGTGTTT      1200
AACCTATGGT AAACAACATG TTAATGAACT ATGCTATCCA TGACTTAATG GACAGTTCAA      1260
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      1320
AAAAA                                             1325

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(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

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Met Lys Leu Leu Leu Trp Ala Cys Ile Val Cys Val Ala Phe Ala Arg
1           5           10           15
Lys Arg Arg Phe Pro Phe Ile Gly Glu Asp Asp Asn Asp Asp Gly His
20          25          30
Pro Leu His Pro Ser Leu Asn Ile Pro Tyr Gly Ile Arg Asn Leu Pro
35          40          45
Pro Pro Leu Tyr Tyr Arg Pro Val Asn Thr Val Pro Ser Tyr Pro Gly
50          55          60
Asn Thr Tyr Thr Asp Thr Gly Leu Pro Ser Tyr Pro Trp Ile Leu Thr
65          70          75          80
Ser Pro Gly Phe Pro Tyr Val Tyr His Ile Arg Gly Phe Pro Leu Ala
85          90          95
Thr Gln Leu Asn Val Pro Pro Leu Pro Pro Arg Gly Phe Pro Phe Val
100         105         110
Pro Pro Ser Arg Phe Phe Ser Ala Ala Ala Ala Pro Ala Ala Pro Pro
115         120         125
Ile Ala Ala Glu Pro Ala Ala Ala Ala Pro Leu Thr Ser Thr Pro Val
130         135         140
Ala Ser Glu Pro Ala Ala Gly Ala Pro Val Ala Ala Glu Pro Ala Ala
145         150         155         160
Glu Ala Pro Val Gly Ala Glu Pro Ala Ala Glu Ala Pro Val Ala Ala

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	165	170	175
Glu Pro Ala Ala Glu Ala Pro Val Gly Val Glu Pro Ala Ala Glu Glu			
180	185	190	
Pro Ser Pro Ala Glu Pro Ala Thr Ala Lys Pro Ala Ala Pro Glu Pro			
195	200	205	
His Pro Ser Pro Ser Leu Glu Gln Ala Asn Gln			
210	215		

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TGCGGGCTCA CANGAANAGT CTCACCTCAG TGCCAAGGGG TGTCAGAGAT GCTCACTGCC	60
CTCCTCTCCT TGGGGTTGCA TGNAGGCATG ATGGCGCTTG GCCGTGGCAG GGTAAGGAAC	120
CGGCGACNGA GGCCCATCAC GTGTTTCACAT GCTCTCCTGC GTCNGTGCTT GGGAGATATG	180
GA CTGTCNTG TCCTTAGACC ACATTTATNT CAAGGCAAGG GGAGC	225

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GGTTCAAAAT GAGGCAAAGA TAGGAAAGTG CTTCTTACAG ATAATTTTCA AGGCCAGTGA	60
CTGGAGAGAG GGGTAGGTCT GTCAATCGAG TGCTTGCTGA CTGCACATAT CACAGGGCGT	120
GTGACGACTG CTGGGAGAGG AAAGCGAGAC ATCATTCCAA CCCTCCAGAA GCTAAAGATC	180
CTGGAACTCA AGGGGAAAAC TAACGTAAGT GCGAAAGCGA ACAAGCAAAC ATGTCCTCAA	240

CGGGGCAGGC AGGCTGTCGG GGTACAGAGC TGGGATCTGG GAAGGAACAG AGAGGGCCGC 300
 TCAGGGAGAG GAAGCACAGT GCCACCGGAG GCACGCACTC AGCAGGCACT CGCAGGCTGG 360
 GCAGAGGTAG AGAAGCAGCG CTGCACAGGC AGGCAGCTGA CCCAGGGCTC TTAGAGCCGG 420
 GCAGGAGAGC TGGTGTGGGA CCTGGGAGGA GGACAGGAGC CTTCAAAGCA GCACCGCCTG 480
 ATTGCAGCCA GGAGGGTAGC ATCAAGGAAG ATGGAAGTGC GGCCAGGCCA CAT 533

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met	Ser	Ser	Thr	Gly	Gln	Ala	Gly	Cys	Arg	Gly	Thr	Glu	Leu	Gly	Ser	1	5	10	15
Gly	Lys	Glu	Gln	Arg	Gly	Pro	Leu	Arg	Glu	Arg	Lys	His	Ser	Ala	Thr	20	25	30	
Gly	Gly	Thr	His	Ser	Ala	Gly	Thr	Arg	Arg	Leu	Gly	Arg	Gly	Arg	Glu	35	40	45	
Ala	Ala	Leu	His	Arg	Gln	Ala	Ala	Asp	Pro	Gly	Leu	Leu	Glu	Pro	Gly	50	55	60	
Arg	Arg	Ala	Gly	Val	Gly	Pro	Gly	Arg	Arg	Thr	Gly	Ala	Phe	Lys	Ala	65	70	75	80
Ala	Pro	Pro	Asp	Cys	Ser	Gln	Glu	Gly	Ser	Ile	Lys	Glu	Asp	Gly	Thr	85	90	95	
Ala	Ala	Arg	Pro	His												100			

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TAGGCAGTCA TCTTTGTAAA CCTCCACTGG TGCTGGCTGC GTTTAGAACA TACTCCATAT	60
AAAACAGGCC CTGGGATTAC AGGCATGAGC TACCGTGCCT GGCCCCCTTT TTTTAAATTA	120
CAGAGAAATA AGTTACACCT TAGTATCAGA TATTAATTTT CTTCAGTGTT CAGGCAATTA	180
GTATTTAGAA AGCTCTTGTC ATGAGATGGC TCTGGGATGT GATGATGATT GTTGGGATTG	240
AAAAAATGGT AGTATCATGG AGAGATCATA ATAAATTCTT AGTATTAAAA GTGGTTTTGC	300
TTTCAGTTAG GGAGAAAAAT TAGATTGTAC TATTTTTCCT CTATGATTTC CTTCAGTTAT	360
CTTCCAAATG TTGTTTTTTC CCCACAGCCC CCTTAACATT GTTCTCTATG CACTTCTCAA	420
TACATTTTCA TTTGTTTCTC AAAAAAAAAA AAAAAAAA	458

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTTTTTTTTT TTTTGTAGA GACAGGTCT TGCCATTTTG CCCAGGTGG TCTCAAACCT	60
CTGAGCTCAG GCTATCTGCC CACCTTGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC	120
CACTGTGCCC GGCTGTATT GTTTAAGTT ACACCTATTC CTTTAAAAAT TCAGAATTTG	180
TTAAGCATTT AAAACAAATT CATAAATTAA AACCTCCTTG AGATACCATT TACCATGTAG	240
TTTGATGAAC ATAATACATG GTGCATTACA TTGGCAAAAG CAGTGGGGAA AAAGATGCTT	300
TTATAAATGT CTGGTGGGAG TTAAATTGTG TAACTTCTAT TACACTTTTG TAATAGCTAC	360
CAAAATATGT TATTTCTATC TACCTCTCTC TCTCTGACTC AACAGTTCCA TTTCTAGGTT	420
TTGTGTTGTG GATATTCTTG AACATTGTGA AATGTATACA GGGAGGCTTC ACAGCAGCAC	480
TGTTTGTTC AAATGATTTG AAAACAACCT CTCCATAAAC GAGATAGGCT AAATCAAGCA	540
TGGCACACCT ATACAATGGA TGCGGCCATT AAAAAGAACA AGGCAGCTCA TATGCATCAA	600
TATAAAAAGG TCTATAAACT ATACTATCAA ATGAAAATAG CAAGATGCTA CCATTTATAT	660
TAAAAAGAGG ACAAATATT AATATATTCA TGGTTGCTTG TCTATGTGGA ATATTTCTGG	720

ATATATACAT AAGAAGTTAC ATTGGTTACC TATGGGCAGG TTACTACTGG GTGGCTTGTG 780
 GGTGAGGGCA GGAAGAGCTT ACTTTCCATG GTAAACCTTT TTGTATATTT TGCAGCATTC 840
 AAAAATTCTA ATTTAAAGTT TATTTTAGAA AAATGCCCCC ATGTATACAA GTGATTTCCA 900
 AGTTCCTCCT TCAATATTTT TAATGATTAT GGAACACACT GAACTTCTTT TTTATTATTC 960
 TAGCTGTGAA CTCTGTCTGC TGTCTACATG CACATATATA ATCTATGTAA TATTTAAATT 1020
 TATATCCTTT ATATGTCAGT TGGGTGGTGA GTAAAAGAAA AATATATTTT TATCAGCAAA 1080
 CTTGGTAAAT TGTTGAGGT TCTGATATAG TCAGAGGTAG TTGCTTATCA CAACATTAGG 1140
 TAAGTTTTTA AARACACCTA TTTAAAACAC ACTGATGTAT ATATATATTG GTCTGTTTTTC 1200
 ATGCTGCTGA TAAAGACATA TCCAAGACTG GGAAGAAAAA GAGGTTTAAT TGGGCTTATA 1260
 GTTCCACATG GCTGGGGAGG CCTCAGAATC ATTGCGGGAG GCAAAGGCA CTTCTTACAT 1320
 GGCAGTGGCA AGAGAAAAAA AAAAAAAAAA 1350

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Leu	Pro	Phe	Ile	Leu	Lys	Arg	Gly	Gln	Asn	Ile	Asn	Ile	Phe	Met
1				5				10						15	
Val	Ala	Cys	Leu	Cys	Gly	Ile	Phe	Leu	Asp	Ile	Tyr	Ile	Arg	Ser	Tyr
			20					25						30	
Ile	Gly	Tyr	Leu	Trp	Ala	Gly	Tyr	Tyr	Trp	Val	Ala	Cys	Gly		
			35					40					45		

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

[illegible]

101

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met	Lys	His	Met	Asn	Thr	Leu	Pro	Ile	Phe	Ser	Ser	Leu	Ile	Ser	Phe	
1				5				10					15			
Leu	Pro	Ala	Val	Ser	Ala	Gly	Arg	Ser	Ala	Ile	Thr	Thr	Leu	Cys	Asn	
			20				25						30			
Ile	Thr	Glu	Gln	Leu	Glu	Val	Leu	Gly								
			35				40									

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CATGGCGTCC AGGTCTAAGC GGC GTGCCGT GGAAAGTGGG GTTCCGCAGC CGCCGGATCC	60
CCCA GTCCAG CGCGACGAGG AAGAGGAAAA AGAAGTCGAA AATGAGGATG AAGACGATGA	120
TGACAGTGAC AAGGAAAAGG ATGAAGAGGA CGAGGTCATT GACGAGGAAG TGAATATTGA	180
ATTTGAAGCT TATTCCTAT CAGATAATGA TTATGACGGA ATTAAGAAAT TACTGCAGCA	240
GCTTTTTCTA AAGGCTCCTG TGAACACTGC AGAACTAACA GATCTCTTAA TTCAACAGAA	300
CCATATTGGG AGTGTGATTA AGCAAACGGA TGTTTCAGAA GACAGCAATG ATGATATGGA	360
TGAAGATGAG GTTTTTGGTT TCATAAGCCT TTAAATTTA ACTGAAAGAA AGGGTACCCA	420
GTGTGTTGAA CAAATTCAAG AGTTGGTTMT ACGCTTCTGT GAGAAGA ACT GTGAAAAGAG	480
CATGGTTGAA CAGCTGGACA AGTTTTTAAA TGACACCACC AAGCCTGTGG GCCTTCTCCT	540

Ile	Gln	Gln	Asn	His	Ile	Gly	Ser	Val	Ile	Lys	Gln	Thr	Asp	Val	Ser	100	105	110	
Glu	Asp	Ser	Asn	Asp	Asp	Met	Asp	Glu	Asp	Glu	Val	Phe	Gly	Phe	Ile	115	120	125	
Ser	Leu	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Gly	Thr	Gln	Cys	Val	Glu	Gln	130	135	140	
Ile	Gln	Glu	Leu	Val	Xaa	Arg	Phe	Cys	Glu	Lys	Asn	Cys	Glu	Lys	Ser	145	150	155	160
Met	Val	Glu	Gln	Leu	Asp	Lys	Phe	Leu	Asn	Asp	Thr	Thr	Lys	Pro	Val	165	170	175	
Gly	Leu	Leu	Leu	Ser	Glu	Arg	Phe	Ile	Asn	Val	Pro	Pro	Gln	Ile	Ala	180	185	190	
Leu	Pro	Met	Tyr	Gln	Gln	Leu	Gln	Lys	Glu	Leu	Xaa	Gly	Ala	His	Arg	195	200	205	
Thr	Asn	Lys	Pro	Cys	Gly	Lys	Cys	Tyr	Phe	Tyr	Leu	Leu	Ile	Ser	Lys	210	215	220	
Thr	Phe	Val	Glu	Ala	Gly	Lys	Asn	Asn	Ser	Lys	Lys	Lys	Pro	Ser	Asn	225	230	235	240
Lys	Lys	Lys	Ala	Ala	Leu	Met	Phe	Ala	Asn	Ala	Glu	Glu	Glu	Phe	Phe	245	250	255	
Tyr	Glu	Lys	Ala	Ile	Leu	Lys	Phe	Asn	Tyr	Ser	Val	Gln	Glu	Glu	Ser	260	265	270	
Asp	Thr	Cys	Leu	Gly	Gly	Lys	Trp	Ser	Phe	Asp	Asp	Val	Pro	Met	Thr	275	280	285	
Pro	Leu	Arg	Thr	Val	Met	Leu	Ile	Pro	Gly	Asp	Lys	Met	Asn	Glu	Ile	290	295	300	
Met	Asp	Lys	Leu	Lys	Glu	Tyr	Leu	Ser	Val							305	310		

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCGGTCCTGC CACACAAGCT GGGCGGCGGA GGCCACGCAG CCGGGCCTTC TTCTCTCTGG	60
GACCCCTCCGC CAGCGCATAG CCGCAGGCCG GTGTGACTTC TGCACCCCTCG GTTCTGAGGG	120
TACGGTGACC CCTAGTGGGC AGTTTGCAAA ATGTGATTCC TTCTTCCCAA CTCCCCATCC	180
CCCCTTCCCT TCCCGTCACG TCCTGTTTGG GGGTTAATTC GGTTTTTTCT CTGTTGCATC	240
GCGCCTACTG TCGTGTGCG ATARCGTGTG TGGGGGTGAG AGTTTGTTTT CTGGAATGGT	300
AGGTGCTGGG AGGAGGAGTT TGATGGAGGG CTTCTGGCT GCTTCTGGCC CTCACCTCGT	360
GGAGGCCTTC ACAGAGACCC TGTGGGCCCT GGCCCTGTGC TGGCACTGTG CCAGTCATGA	420
GGCAGCTCTG ATCACTTCCC CACTGTGGAA ACAGGACTGA CCCAGCCTTC AGTGTGGGCT	480
GCTGAAGCTA TCCTCCTCAG GCCTCAGGGA TGACCTCCTG CCTGAGCCTC TCACAGGCTG	540
GCTGTGGGCC AGTTTCATCT GCTTTCCTGT TGGGGGTCCC GGGCCTCTGC TGTCTTGAC	600
CCACTGGTGT TCTGTGCAAG GCTTCTTCCC ATTCACCAAG TGCACACCTT GCATCTGCCG	660
CTCGGCATGC ACCAGTTCCA CACACCATCC CATTTTACAG ACAAGGACGC TGAGGCCTGC	720
AGCAGCAGTG TGA CTTGCTC AAGGTCCAGT GAGTGACCTC ATTCCCCAGA AAAGGCTCCT	780
CCCACACCAG AGTACAGCCT GGGTAGGGGG AAAATCAGTT CTTTCAGCTA CCACCCATCC	840
AACCTTTGGG CCTATGTGAA AAGAAAGGAA CTAAGCTGGG TGTGTTCTGT CTGGACCTGG	900
GGAGGCCCTT GAAGGCAAAG AGGGAAACTG TCCCAGCTGT TCTGTCCTAG GGGAGGGGGA	960
CATAGCCCTA GCAGGAGCTC CCAGCCCCTC TTGGCACTCT GACACACAAG TACACCCATC	1020
TGGGGCCCGC TTTGCCACGA AGAGCTGGGC AGGCCTGCAG GGTGTGGGGA AGGAGGACAC	1080
AACCTCAAGA AAGGAAGCGT GAACCCAGG GAACAGCGGG TCCCTTCCCT CCTCAGACAC	1140
AAGCCACCTC AGCTTGTGGC TCTTGCCCC CAGCCCCACC AACCCACCTG TTCATTTATT	1200
CAACAGACAA TGACAGCTGA TATTTATTGG ACATTTGCAC CATGCCAAGC ATTGGGCTTG	1260
GATTATCCCA TTTGTTTCTC ACAGCCGTA TTTATTGTCT GCTCCTCTGT GCCAGGTGCT	1320
GTGCTCTGGG CAGGGGCACT GCATGGGCTG CCTGCCCTGG TGGAGCTTGT GGTCTGATGG	1380
GTGAGGCTGA CCAAGCCCA CCCCATTGCC AACAGGGCCA GGGCAAGAGT ACACACAGGG	1440
GCCTCATACC ATATGTCTAA ATATTTAAAA GTTATCAATC AAGCTAACA CTGTAAATA	1500
AAATATGTTT TATTCTCCTA CTTTGAAAAA AAAAAAAAAA AAAA	1544

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met	Pro	Ser	Ile	Arg	Leu	Gly	Leu	Ser	His	Leu	Phe	Leu	Thr	Ala	Gly
1				5				10						15	
Ile	Tyr	Cys	Leu	Leu	Leu	Cys	Ala	Arg	Cys	Cys	Ala	Leu	Gly	Arg	Gly
			20					25					30		
Thr	Ala	Trp	Ala	Ala	Cys	Pro	Gly	Gly	Ala	Cys	Gly	Leu	Met	Gly	Glu
		35					40						45		
Ala	Asp	Pro	Ser	Pro	Pro	His	Cys	Gln	Gln	Gly	Gln	Gly	Lys	Ser	Thr
	50					55					60				
His	Arg	Gly	Leu	Ile	Pro	Tyr	Val								
65					70										

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CNATGCAGGTC TAACTCCTCC ACTCTGGG

29

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TNAGTTTGGTG CTCTGCTCTG ATATTGAC

29

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GNCATCAATAT CCTTACGGTC TCCGAAGC

29

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GNAAATAGGAA CTTTCATGAG AATCAGGA

29

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ANACAATGCAG GCCCAAAGGA GAAGCTTC

29

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GNTTGCTTGTT CGCTTTCGCA CTTACGTT

29

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ANTGGTAGCAT CTTGCTATTT TCATTGTA

29

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TNGGAAGTGTG TTCATGTGTT TCATTGTT

29

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GNCCTCGTCCT CTCATCCTT TTCCTTGT

29

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ANCACCTGGCA CAGAGGAGCA GACAATAA

29

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCGAGCCTT TGAGGGGAAC GACTTGTCGG AGCCCTAACC AGGGGTATCT CTGAGCCTGG 60
 TGGGATCCCC GGAGCGTCAC ATCACTTTCC GATCACTTCA AAGTGTAAGG GGGGCCCTAC 120
 TGACCCTTGG AATTTAGGGG GGCTACCCTA GGCGGCATCC ACAACAGAGA GAATTCCTT 180
 GGAGAGGGGA CCCTGGTGCT CGGCTGTCCC TCTCATCCGC GTAGAAAGTC CCTCATCTGG 240
 GGGCTCCCGA ACTCAGCCCT CTCACATTGT GGCCGGCTTT ACTGACCCTC ACAGACCCAG 300
 GCTGGGCCCT CCCGATAGAG GCCAGCCAAA GGTTCACTCA GCCTCTCTTT CAAGGCTGGT 360
 GTATCTCTAA ATCTTAGACC CTCCTCCGTT ACCGTCAGCC AGGTGGGATG CCCACGTTTT 420
 GGAGAGAAAC CGTTCTGAGG AACCCGGGCC TCTGGGTCCC AGCTGGCTCT CCGGCCCCCA 480
 GGTATGTAT TCTGGGTTGG CCACAAACAG TGGAATTCTA GGCACTCCCG GGACAGGGTG 540
 GGACTGCTGT CCTCATTCAT GCAACCAGCA AATATTCACG GCACCTTGTT TGTGCCAGAC 600
 AGCAGACCGA GGACACGGTT GTTACCAAGA CCAGGCTGTT GCCTTGGAAG AGCCCAGAGC 660

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GTGTCAAGGG AGACAGCCAC ATCACGCCAG AAATACATGA CAGCTGGATT AGCCCTGGGA 720
GAGGGAGGCC CAGATGTGGG AGCTCAGGGG AGGTGCAGCT CAACGTGGAG TTTGGAGGAG 780
GCTACCTTGA CCTTTGAATG CCAAGTGGGA GCCAGCCAGA TGAAAGGGGT TAAAACTAA 840
TATTTATATG ACAGAAGAAA AAGATGTCAT TCCGTAAAGT AAACATCATC ATCTTGGTCC 900
TGGCTGTTGC TCTCTTCTTA CTGGTTTTGC ACCATAACTT CCTCAGCTTG AGCAGTTTGT 960
TAAGGAATGA GGTTACAGAT TCAGGAATTG TAGGGCCTCA ACCTATAGAC TTTGTCCCAA 1020
ATGCTCTCCG ACATGCAGTA GATGGGAGAC AAGAGGAGAT TCCTGTGGTC ATCGCTGCAT 1080
CTGAAGACAG GCTTGGGGGG GCCATTGCAG CTATAAACAG CATTAGCAC AACACTCGCT 1140
CCAATGTGAT TTTCTACATT GTTACTCTCA ACAATACAGC AGACCATCTC CGGTCCTGGC 1200
TCAACAGTGA TTCCCTGAAA AGCATCAGAT ACAAATTGT CAATTTTGAC CCTAACTTT 1260
TGGAAGGAAA AGTAAAGGAG GATCCTGACC AGGGGGAATC CATGAAACCT GTGATATTCT 1320
TGCCCTTTAC AATACAGCAC TGAAGCCAGG ACATGCAGCT GCATTTTCAG AAGATTGTGA 1380
TTCAGCCTCT ACTAAAGTTG TCATCCGTGG AGCAGGAAAC CAGTACAATT ACATTGGCTA 1440
TCTTGACTAT AAAAAGGAAA GAATTCGTAA GCTTTCCATG AAAGCCAGCA CTTGCTCATT 1500
TAATCCTGGA GTTTTTGTTG CAAACCTGAC GGAATGGAAA CGACAGAATA TAACTAACCA 1560
ACTGGAAAAA TGGATGAAAC TCAATGTAGA AGAGGGACTG TATAGCAGAA CCCTGGCTGG 1620
TAGCATCACA ACACCTCCTC TGCTTATCGT ATTTTATCAA CAGCACTCTA CCATCGATCC 1680
TATGTGGAAT GTCCGCCACC TTGGTTCCAG TGCTGGAAAA CGATATTAC CTCAGTTTGT 1740
AAAGGCTGCC AAGTTACTCC ATTGGAATGG ACATTTGAAG CCATGGGGAA GGACTGCTTC 1800
ATATACTGAT GTTTGGGAAA AATGGTATAT TCCAGACCCA ACAGGCAAAT TCAACCTAAT 1860
CCGAAGATAT ACCGAGATCT CAAACATAAA GTGAAACAGA ATTTGAACTG TAAGCAAGCA 1920
TTTCTCAGGA AGTCCTGGAA GATAGCATGC GTGGGAAGTA ACAGTTGCTA GGCTTCAATG 1980
CCTATCGGTA GCAAGCCATG GAAAAAGATG TGTCAGCTAG GTAAAGATGA CAACTGCCC 2040
TGTCTGGCAG TCAGCTTCCC AGACAGACTA TAGACTATAA ATATGTCTCC ATCTGCCTTA 2100
CCAAGTGTTT TCTTACTACA ATGCTGAATG ACTGGAAAGA AGAACTGATA TGGCTAGTTC 2160
AGCTAGCTGG TACAGATAAT TCAAACTGC TGTTGGTTTT AATTTTGTA CCGTGGCCT 2220
GATCTGTAAT TAAACTTAC ATTTTCAAT AGGAAAAAAA AAAAAAAAAA A 2271

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(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```

Met Ser Phe Arg Lys Val Asn Ile Ile Ile Leu Val Leu Ala Val Ala
 1             5             10             15

Leu Phe Leu Leu Val Leu His His Asn Phe Leu Ser Leu Ser Ser Leu
      20             25             30

Leu Arg Asn Glu Val Thr Asp Ser Gly Ile Val Gly Pro Gln Pro Ile
      35             40             45

Asp Phe Val Pro Asn Ala Leu Arg His Ala Val Asp Gly Arg Gln Glu
      50             55             60

Glu Ile Pro Val Val Ile Ala Ala Ser Glu Asp Arg Leu Gly Gly Ala
      65             70             75             80

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Ile Ala Ala Ile Asn Ser Ile Gln His Asn Thr Arg Ser Asn Val Ile
85 90 95

Phe Tyr Ile Val Thr Leu Asn Asn Thr Ala Asp His Leu Arg Ser Trp
100 105 110

Leu Asn Ser Asp Ser Leu Lys Ser Ile Arg Tyr Lys Ile Val Asn Phe
115 120 125

Asp Pro Lys Leu Leu Glu Gly Lys Val Lys Glu Asp Pro Asp Gln Gly
130 135 140

Glu Ser Met Lys Pro Val Ile Phe Leu Pro Phe Thr Ile Gln His
145 150 155

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

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GCCGACCGAA GAGGCTGGAC ATGACACCAG TGGCATATCA CGGCCATGGG GTCTCAGCAT 60
TCCGCTGCTG CTCGCCCCCTC CTCCTGCAGG CGAAAGCAAG AAGATGACAG GGACGGTTTG 120
CTGGCTGAAC GAGAGCAGGA AGAAGCCATT GCTCAGTTCC CATATGTGGA ATTCACCGGG 180
AGAGATAGCA TCACCTGTCT CACGTGCCAG GGGACAGGCT ACATTCCAAC AGAGCAAGTA 240
AATGAGTTGG TGGCTTTGAT CCCACACAGT GATCAGAGAT TGCGCCCTCA GCGAACTAAG 300
CAATATGTCC TCCTGTCCAT CCTGCTTTGT CTCCTGGCAT CTGGTTTGGT GGTTTTCTTC 360
CTGTTTCCGC ATTCAGTCCT TGTGGATGAT GACGGCATCA AAGTGGTGAA AGTCACATTT 420
AATAAGCAAG ACTCCCTTGT AATTCTCACC ATCATGGCCA CCCTGAAAAT CAGGAACTCC 480
AACTTCTACA CGGTGGCAGT GACCAGCCTG TCCAGCCAGA TTCAGTACAT GAACACAGTG 540
GTGAATTTTA CCGGGAAGGC CGAGATGGGA GGACCGTTTT CCTATGTGTA CTTCTTCTGC 600
ACGGTACCTG AGATCCTGGT GCACAACATA GTGATCTTCA TGCGAACTTC AGTGAAGATT 660
TCATACATTG GCCTCATGAC CCAGAGCTCC TTGGAGACAC ATCACTATGT GGATTGTGGA 720
GGAAATTCCA CAGCTATTTA ACAACTGCTA TTGGTTCTTC CACACAGCGC CTGTAGAAGA 780
GAGCACAGCA TATGTTCCCA AGGCCTGAGT TCTGGACCTA CCCCCACGTG GTGTAAGCAG 840
AGGAGGAATT GGTTCACCTA ACTCCCAGCA AACATCCTCC TGCCACTTAG GAGGAAACAC 900
CTCCCTATGG TACCATTTAT GTTTCTCAGA ACCAGCAGAA TCAGTGCCTA GCCTGTGCC 960
AGCAAATAGT TGGCACTCAA TAAAGATTTG CAGAATTTAA TACAGATCTT TTCAGCTGTT 1020
CTTAGGGCAT TATAAATGGA AATCATAACG TGGTTCTAGG TTATCAAACC ATGGAGTGAT 1080
GTGGAGCTAG GATTGTGAGT GACCTGCAGG CCATTATCAG TGCCCTCATCT GTGCAGAAGT 1140
GGCAGCAGAG AGGGACCATC CAAATACCTA AGAGAAAACA GACCTAGTCA GGATATGAAT 1200
TTGTTTCAGC TGTTCCCAAA GGCCTGGGAG CTTTTTGAAA AGAAAGAAAA AAGTGTGTTG 1260
GCTTTTTTTT TTTTATAGAA GTTAGAATTG TTTTACCAA GAGTCTATGT GGGGCTTGAT 1320
TCACCCCTCA TCCATTGGCT GGAACATGGA TTGGGGATTT GATAGAAAAA TAAACCCTGC 1380
TTTTGATTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA 1425

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(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg
 1              5              10              15

Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu
      20              25              30

Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser
      35              40              45

Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln
      50              55              60

Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg
      65              70              75              80

Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu
      85              90              95

Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu
      100             105             110

Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln
      115             120             125

Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn
      130             135             140

Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln
      145             150             155             160

Tyr Met Asn Thr Val Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly
      165             170             175

Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val
      180             185             190

His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile
      195             200             205

Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys
      210             215             220

Gly Gly Asn Ser Thr Ala Ile
```


(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

CTTCCAAAGA GCGACTCTTA CTGTTTCTCA TGGTGAGAAG ACAATATTTG CTTTCTCTTT      60
TTCCTTTCTT CCGGATGAGA GGCTAAGCCA TAATAGAAAG AATGGAGAAT TATTGATTGA      120
CCGTCTTTAT TCTGTGGGCT CTGATTCTCC AATGGGAATA CCAAGGGATG GTTTTCCATA      180
CTGGAACCCA AAGGTAAAGA CACTCAAAGA CAGACATTTT TGGCAGAGCA TAGATGAAAA      240
TGGCAAGTTC CCTGGCTTTC CTTCTGCTCA ACTTTCATGT CTCCCTCCTC TTGGTCCAGC      300
TGCTCACTCC TTGCTCAGCT CAGTTTTCTG TGCTTGGACC CTCTGGGCCC ATCCTGGCCA      360
TGGTGGGTGA AGACGCTGAT CTGCCCTGTC ACCTGTTCCC GACCATGAGT GCAGAGACCA      420
TGGAGCTGAA GTGGGTAAAGT TCCAGCCTAA GGCAGGTGGT GAATGTGTAT GCAGATGGAA      480
AGGAAGTGGA AGACAGGCAG AGTGCACCGT ATCGAGGGAG AACTTCGATT CTGCGGGATG      540
GCATCACTGC AGGGAAGGCT GCTCTCCGAA TACACAACGT CACAGCCTCT GACAGTGGAA      600
AGTACTTGTG TTATTTCCAA GATGGTGACT TCTATGAAAA AGCCCTGGTG GAGCTGAAGG      660
TTGCAGCACT GGGTTCTAAT CTTACGTCG AAGTGAAGGG TTATGAGGAT GGAGGGATCC      720
ACCTGGAGTG CAGGTCCACC GGCTGGTACC CCCAACCCCA AATACAGTGG AGCAACGCCA      780
AGGGAGAGAA CATCCCAGCT GTGGAAGCAC CTGTGGTTGC AGACGGAGTG GGCCTATATG      840
AAGTAGCAGC ATCTGTGATC ATGAAAGGCG GCTCCGGGGA GGGTGTATCC TGCATCATCA      900
GAAATTCCCT CCTCGGCCTG GAAAAGACAG CCAGCATTTT CATCGCAGAC CCCTTCTTCA      960
GGAGCGCCCA GCCCTGGATC GCAGCCCTGG CAGGGACCCCT GCCTATCTTG CTGCTGCTTC     1020
TCGCCGGAGC CAGTTACTTC TTGTGGAGAC TACAGAAGGA AATAACTGCT CTGTCCAGTG     1080
AGATAGAAAG TGAGCAAGAG ATGAAAGAAA TGGGATATGC TGCAACAGAG CGGGAAATAA     1140
GCCTAAGAGA GAGCCTCCAG GAGGAACTCA AGAGGAAAAA AATCCAGTAC TTGACTCGTG     1200

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

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AATGGTTCCA GCCTTAATGG AGAAGCCAGT TTCTTTTTTC TTGTTGTTTT ATTGTTTTTA 60
AGCCTCTCTC TGGTTTTTCAG TAGAGTTTGA CCTTAAATAT CATCTTTGAT TACTATTGGT 120
GTCCTTGTA TAGGTTCTT TGCAAAAGTT TGAGTGCAAG TTTTAAGCTA AAAACACGTT 180
TTTAAACTTT CACAAATTTT GTAAGATGAC AATAGCATTG TGTAACATAG ACATTATGGT 240
AATAGTGATT TTCTCTCCAT CCCTATTTTG TCCAGCGATT TCCAAGTTAT AAGACGTGAA 300
TAAGACTAAC CGCTCACTTC CACCAGCAGC TGACCTGGTG GGCTTTTGAG TTCAAAGAGT 360
CATTTCTTCA TCTTACCTCC AGCACTGCAG GGCCGTGTGA CCTTGCAGAG CCTTGTCTCT 420
CATTGATGAA AGGAGCTCAT GCCTCATGAA GCCACTGGTA AGGGCCATGG AGCTCACGGG 480
CCATCAAGCT TCCTTCCCAT CACTTGTTGGG TGGAATTGAC ATTACCCGAT GAGCTCTTCC 540
TGGGGTCACC TGGGAGGGAG TGGCCCATGG GTGGTATGAC AAAATCTCAT AGTCAGTCTT 600
TGCAGTTTTT TCCACAGGTA AAATGAGATT TTGGAAAATT TTCATTTGTT TGTATTTGTC 660
CCAAGGTGAG TCTTACATAT TTTGAGCAAC AAAACGAAGA TCATTATGAA AATGTCCTTA 720
TGGAAGCACT CTAGGGCCAT TGCTCATTTT TATGAGTCCT CGTGCTAAGT CCCTGAGTAC 780
TGTGGCTCAT GTCTTAGCTG GCTAAATCAC AGTCAAAATT CTCTTCTTAA GCCTCAAAAT 840
AAGCTGCTGA TTATACTGCC TGTTGGCCAG ACTAATCAAA TACATTTGAT GTTTTAGCTG 900
ACTCCAGATA CTTTTCTTTC CTCTCTCTTG GTTCTTTAAC TGTCATCCCA GATCTGCGAC 960
ATGCAATAAG GAAAAGTGGT TCAGGGAGGA AGTAGGATTC CTTTGTGCTG TAGGAACCAC 1020
GTTAGCTTTG GATTGTCCAT AGAATGCACC CTTAACAGTT CTTGGAAAAT GGATGATATT 1080
TGGTTCTCTG CCCATGTTCA GTGTTCTTTG GCAGCTGCAA AGCATATCCT AGCTAGAATC 1140
CTTATCGTCT TGAAGTTCAT CAAAGATTTT GAACAGTCAT GGTGGAGATA CAACCTAAGT 1200
ACATTCATGC CCATTGAGAC AATCCTTTGG TTTGAGCGAC GGAAGGAGGA ATAAACACAT 1260
GAATGTATTT TATTGAATCC CAGAGACCTT AACACACCAA GACTCATTAA TATATGCATA 1320
CATGGATGGC AGAATAATAA ACCTCACCTG ACCTGTCAGT GTACTCTCAG TTTTAAAGGT 1380
TCTCCCAAAA CAGGGGAACT GAAAAATACT TGGGCAGAAA GAAAATATCA TCAAATAACA 1440
CCTATTTCTT TTCAGCTATA GAGATGGCTG GATATCAAAA GCACCACGGG AGCTTTGCAA 1500
TTTGCTGCTC TTTTCAGCCC TCAGCTTGAC TCTCAGTTTT CAAGAGGGAG AAAATGAATG 1560
TTTCCCAGCA TTCTCTGTCC TTTGCTCCAA AGAAGAGAGC AGGTGTTGGC TTCCAAACCT 1620
TCCGTATTTT CTTATTGCTG TTAGGGGGAT CAACTGCATG TTTCTGAGG GAAAAGGGTG 1680
GCTCACTGAC CTACTTGAAG GCATTCTCTC AGTGGAAGCT GGGCAAGAGA ATCCAGGGAT 1740
TTCTTTTGCA GGTTCCTGCG CAGTGCCCCC GCCATCAAGC TGCCATAAAT GTGAATATTG 1800
CTTCCCTGCG TTTGAGAGGT GGTAATATTG GGGCAAGTGG TGGAGGATCT AAAAAAAAAA 1860
AAAAA 1865

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(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

Met Asn Val Ser Gln His Ser Leu Ser Phe Ala Pro Lys Lys Arg Ala
 1             5             10             15

Gly Val Gly Phe Gln Thr Phe Arg Ile Phe Leu Leu Leu Gly Gly
          20             25             30

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Ser Thr Ala Cys Phe Leu Arg Glu Lys Gly Gly Ser Leu Thr Tyr Leu
35 40 45

Lys Ala Phe Ser Gln Trp Lys Leu Gly Lys Arg Ile Gln Gly Phe Leu
50 55 60

Leu Gln Val Ser Ala Gln Cys Pro Cys His Gln Ala Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TATGTATTTG ACAGCATGGT ATAATGAAAA GAGCAGTTGG ACCAGAAGGT AAATTCTAGT 60
CCAGATTTTG ACATTTAGAT GTGTATATAT GGGAAAGTTT CTTAAACTT CGAGTTAATT 120
TTTCTCATCT GTGAAATAAA GGGATTGGAC TAGATACTCT TTAATAGATA TTCCTTATAT 180
GCTTGCTCTC TTCTAGGTCT AAAATTCTGA TCCTTTAGTA GTTTATAAAT GATTATTGGT 240
ATCATTTTCA TCATTTTAGG AGCTCTTTTT TAAAAAATTA TTATTATTTT TTTTGCTCTG 300
TAGCCCATTT CTAGAACATC TTGGGAGTTC TAATTATGTT TTAGATAACA TAAAAAGCAT 360
AGAATCAGAC ATAGTTAAGC AAGAATTTCA CTTAGTTCCC TAGTTTTTAC AGTCTAAATA 420
CATTTTTCTT TCTTTAAAC TGGAGGTAC TGATACCACC ATTTTCGTCA CCAACAGCCT 480
AATAATTCAC AAAGCTATTT GCTAATTTTT GACACTTTTT TCTTTGCCAG TACCATTAAAG 540
GGATTGAAT TTTTTGAGG TTCCATGTTT ATTTCTTTAG TTATGAGTAT GACCTTGGAC 600
AAGTTACTTC TCTGTACCTG TAAAGTGAGA GTAAAATAAC ATCTAGTTCA TAGGGTTGTT 660
GACTAGTACC TGGCCCATGG TAATCACTGT GTCATGTTGG CTGTTACTAC CCTTTAACAT 720
GATTTGCTCC CCTCCCTGTG GTAAAAAGTA TTCATTGGCA CTACTAATTA ATCTGTTAGC 780
TCAACATATA CTAACCAAAA TGGAAATTTG TTTTGTGAAA TACAATTGTC AGTTCCTTTT 840
CATTATAAGA AACGTTAGTT TATTAGTAGT ATATACCCCT GAGAAAGCAC TAATTTATTT 900
TGAAATTGAG TGGATTAATT CATAATATGA AAGCTGAGAA TGTAGATTGT CTTCTTTCTC 960
TATTTTGAAT AGTTCATAGA ATAATTTATT TCTTTTATCT GGAACAAAA ATAACGGTTC 1020
TAATTTGTGA CATTCTCAA CATATTTTAC AAGTTTAGAT AAGTTGAGAA TGGCAAAAAC 1080
CACAAATTACT TTTGCAACAA TCTAATACTT TTAGAAGAAA AATCTATCTT ACCTTATTTT 1140
TACTATAAAA AAAAAAAAAA GGCCAAAGAG GCCTACAGGA TTTTGAGATG GAGGAACACA 1200
TATTTAATTC CCCTTTATGC CTGGTTCTT GCTCCTCTTT CCACGTTGGA TAACAATTTT 1260
TTGGTTGTTT TGTTTAAGTT GGTGCTCTGA AGCTTAATCT CAGTACCCCT TACTCTGAAT 1320
TGTCAAATTT TGATAAACG TGCCATTTTC TTTGGTAAGA GAAAGCAGGT CTTAATGTCT 1380
GCCAGAACAC AATTTATATG CCTTATTGGC TTCATTAAAC TTTTAGAAAA CTTTAGCATT 1440
TGTTACTTTT TTCCATTGCA TTTACTTTCA AATGCACCTA ATGAATTCGT CACCCAGTCG 1500
CAACTTTTCC CTTCTCTGTC CCATTGCTTT CTCCTTTCCC CGACGCACAG AATAAACATG 1560
AAGCTCAGCA GTAGAAGCGT AATGATTTCC CTCAGGAAAA ACTTCTGACA GCTAGGTTTT 1620
TCAAGGGTTT CCCTGTGCTA GCTGAGATGC AAAACAAATC ATGGAAGATT GCATACCTGT 1680
GTGGTATTTT AAAACAAGT TGACTTTTTC AGTTTCTTGA ACGGTAAAGG GTGGATTTAA 1740
AAACTAGACA GTTTAGTTTT GGGGAACAGA AGCTCTCTTC GTCTTAAGCC AGATTCTCTG 1800
ATTCTTTTAG ACGTCATAGC TCCTTAGTTC TGCTCCTGTC GCCCTAACTT GGCATGGGCA 1860
AGTTGAAGTT CATCCTTAGA CTGCAGCGTT CTGAGCATGG CTGAAGTATT AAAATGTTTA 1920

ATATTTTTTA GAGCAAAATT GATGGAAAGC ATTTGGCTGA ATCTAAAGAC CTGCAGTCAG 1980
 ATTCTTCAAT GTGGTTTACC CAACTGGAGT AGTGATAAAC ACCTTAATCA TAAAATGAAT 2040
 AAAACAAAA AAACCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 2094

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met	Ser	Ala	Arg	Thr	Gln	Phe	Ile	Cys	Leu	Ile	Gly	Phe	Ile	Lys	Leu
1				5					10					15	
Leu	Glu	Asn	Phe	Ser	Ile	Cys	Tyr	Phe	Phe	Pro	Leu	His	Leu	Leu	Ser
		20					25						30		
Asn	Ala	Pro	Asn	Glu	Phe	Val	Thr	Gln	Ser	Gln	Leu	Phe	Pro	Ser	Leu
		35					40					45			
Ser	His	Cys	Phe	Leu	Leu	Ser	Pro	Thr	His	Arg	Ile	Asn	Met	Lys	Leu
	50					55					60				
Ser	Ser	Arg	Ser	Val	Met	Ile	Ser	Leu	Arg	Lys	Asn	Phe			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AAATTCAACA TAAACCCAAA TCTGTACTTC TCCAGAGGAG CAGCTCTGAG GTAGAAATTA 60
 CAACGATGAA AAGAGCACAA CGTACAAAAC CAAGAAAGAG TCTGTTGTGT GAAGGGTCAT 120
 TCGATGAAGA AGCTTCTGCA CAGTCCTTTC AGGAAGTGTT AAGTCAATGG AGAACCGGAA 180
 ATCATGATGA CAACAAGAAA CAGAATTTC ATGCAGCAGT AAAAGACTCA TTGGAAGAAT 240
 GCGAAGTACA GACTAATCTG AAAATTTGGA GAGAACCACT TAATATTGAA CTTAAAGAAG 300
 ACATTCTATC CTATATGGAA AAATTATGGC TTAATAAACA CAGGAGAACT CCACAAGAGC 360
 AACTTTTTTA AATGCTACCA GATACGTTCC CACATCCACA TGAAACCACT GGTGATGCAC 420

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AGTGTTCCTCA AAATGAAAAC GATGAAGATA GTGATGGTGA GGAGACCAAA GTACAACACA 480
CAGCTCTTTT ATTGCCAGTA GAAACATTAA ACATAGAGAG ACCTGAACCA TCTCTAAAGA 540
TAGTCGAACT GGATGATACT TATGAAGAGG AATTTGAAGA AGCAGAAAAAT ATTGTGCCTT 600
ACAAAGTTAA ATTAGCTGAT GCAGACAGTC AACGAAGTTG TGCTTTTCAT GATTGTCAGA 660
AGAATAGCTT TCCATATGAA AATGGCATCC ATCAACATCA TGTTTTTCGAT AAGGGAAAAG 720
GAGACTTCTT AAATCTTTGT CTGAGAAAACA GCTATACTTA TTATAAAGAT AATTCAAAAG 780
CAGAACTTC AAACACAGAT TTTGACAACA TCGTGGATCC TGATGTGTAT TCTTCTGACA 840
TTGAAAAAAT TGAGGAAAGC ACCTCCTTTG AAAGAAATTT AAAGGAGAAA AATATAGGTT 900
TAGAAAGTAA TCAAAAGTCT GATGATTCCCT GTGTATCACT TGAAAGCAAG GACACTTTGC 960
TAGGTAGAGA TTTAGAAAAA GCTCCCATTG AGGAGAAATT ATCTCAAGAC ATCAAGAAGT 1020
CCTTGGAATT GAGCAATCTG TATAAGAGGC CAAGCTTTGA AGAATCAAAA ACTACAAAAGT 1080
CATCACTGTT GTTACAAGAA ATAGCCTGCA GAAGTAAGCC TATAACAAAA CAATATCAAG 1140
GACTTGAGAG ATTCTTTATT TTTGATACAA ATGAAAGACT CAACTTACTT CCTTCTCATC 1200
GTTTAGAATG CAACAATTCC AGTACTAGGA TTACACTTGC AGAAGACAGA GAATGGATTC 1260
CAGACCATAG CTTAAGTGAA TATGCTGATA ATGCAATTGT CTTGGGTGTT CTGCAGGGTG 1320
CTCAGAGTCC ATCATCAAGT AGAAAACAGC AAAAGATGGG TCAGAAATCA CAGAGACCTT 1380
CAACAGCAAA TTTTCCACTT TCCAACCTCTG TTAAAGAAAG CTCCAGTTGC CTTTCATCCT 1440
CTCATCCTCG ATCAAGAAGT GCAGCTGCTC AATCATCATC TAGAGCTGCT TCTGAAATTT 1500
CAGAAATTGA ATATATTGAT ATTACTGACC AGAATGAGCT TTCCTTAGAT GACACTACTG 1560
ATCAACATAC TTTAGACAAT TTGGA AAAAG AATTACAAGT GCTGAGATCT CTTGCAGATA 1620
CTTCAGAAAA GCTTTACAGC TTAACCTCAG AAGAGTTCCC AGATTTCAGC AGCCAATCAC 1680
TGAATATAAG TCAGATTTCC ACAGATTTCC TTAAGACCTC ACATGTGAGG GGTCCCCTGTG 1740
GAGTTGAGGA ATTGAGCTGT TCTGGAAGAG ATACCAAAAT TCAGTCTTTG CTGTCACTTT 1800
CTGAGAGCAG TACAGATGAG GAGGAGGAAG ATTTTCTCAA CAAGCAACAT GTCATCACAC 1860
TACCGTGGTC AAAGAGTACT TAAAGATTAT TTGTTTCTCAA CTGTTTCCAT TTTGTACCCA 1920
GAGTAAAGCA AACAAGTCTG AAAAGTAACC AAGTGATTAC CTATCCAAGT GCTGGAGATT 1980
TTGATTACTA ATGTCTTTGA TGTTTCAAGG CTACAACTA ATAAAAGTAA AATTATAAGT 2040
TCAAAAAAAA AAAAAAAA AAAAAAAA 2069

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(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 605 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

Met Lys Arg Ala Gln Arg Thr Lys Pro Arg Lys Ser Leu Leu Cys Glu
 1             5             10             15

Gly Ser Phe Asp Glu Glu Ala Ser Ala Gln Ser Phe Gln Glu Val Leu
 20             25             30

Ser Gln Trp Arg Thr Gly Asn His Asp Asp Asn Lys Lys Gln Asn Leu
 35             40             45

His Ala Ala Val Lys Asp Ser Leu Glu Glu Cys Glu Val Gln Thr Asn
 50             55             60

Leu Lys Ile Trp Arg Glu Pro Leu Asn Ile Glu Leu Lys Glu Asp Ile
 65             70             75             80

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Leu Ser Tyr Met Glu Lys Leu Trp Leu Lys Lys His Arg Arg Thr Pro
 85 90 95
 Gln Glu Gln Leu Phe Lys Met Leu Pro Asp Thr Phe Pro His Pro His
 100 105 110
 Glu Thr Thr Gly Asp Ala Gln Cys Ser Gln Asn Glu Asn Asp Glu Asp
 115 120 125
 Ser Asp Gly Glu Glu Thr Lys Val Gln His Thr Ala Leu Leu Leu Pro
 130 135 140
 Val Glu Thr Leu Asn Ile Glu Arg Pro Glu Pro Ser Leu Lys Ile Val
 145 150 155 160
 Glu Leu Asp Asp Thr Tyr Glu Glu Glu Phe Glu Glu Ala Glu Asn Ile
 165 170 175
 Val Pro Tyr Lys Val Lys Leu Ala Asp Ala Asp Ser Gln Arg Ser Cys
 180 185 190
 Ala Phe His Asp Cys Gln Lys Asn Ser Phe Pro Tyr Glu Asn Gly Ile
 195 200 205
 His Gln His His Val Phe Asp Lys Gly Lys Arg Asp Phe Leu Asn Leu
 210 215 220
 Cys Leu Arg Asn Ser Tyr Thr Tyr Tyr Lys Asp Asn Ser Lys Ala Glu
 225 230 235 240
 Thr Ser Asn Thr Asp Phe Asp Asn Ile Val Asp Pro Asp Val Tyr Ser
 245 250 255
 Ser Asp Ile Glu Lys Ile Glu Glu Ser Thr Ser Phe Glu Arg Asn Leu
 260 265 270
 Lys Glu Lys Asn Ile Gly Leu Glu Ser Asn Gln Lys Ser Asp Asp Ser
 275 280 285
 Cys Val Ser Leu Glu Ser Lys Asp Thr Leu Leu Gly Arg Asp Leu Glu
 290 295 300
 Lys Ala Pro Ile Glu Glu Lys Leu Ser Gln Asp Ile Lys Glu Ser Leu
 305 310 315 320
 Glu Leu Ser Asn Leu Tyr Lys Arg Pro Ser Phe Glu Glu Ser Lys Thr
 325 330 335
 Thr Lys Ser Ser Leu Leu Leu Gln Glu Ile Ala Cys Arg Ser Lys Pro
 340 345 350
 Ile Thr Lys Gln Tyr Gln Gly Leu Glu Arg Phe Phe Ile Phe Asp Thr
 355 360 365
 Asn Glu Arg Leu Asn Leu Leu Pro Ser His Arg Leu Glu Cys Asn Asn
 370 375 380

Ser Ser Thr Arg Ile Thr Leu Ala Glu Asp Arg Glu Trp Ile Pro Asp
 385 390 395 400
 His Ser Leu Ser Glu Tyr Ala Asp Asn Ala Ile Val Leu Gly Val Leu
 405 410 415
 Gln Gly Ala Gln Ser Pro Ser Ser Ser Arg Lys Gln Gln Lys Met Gly
 420 425 430
 Gln Lys Ser Gln Arg Pro Ser Thr Ala Asn Phe Pro Leu Ser Asn Ser
 435 440 445
 Val Lys Glu Ser Ser Ser Cys Leu Ser Ser Ser His Pro Arg Ser Arg
 450 455 460
 Ser Ala Ala Ala Gln Ser Ser Ser Arg Ala Ala Ser Glu Ile Ser Glu
 465 470 475 480
 Ile Glu Tyr Ile Asp Ile Thr Asp Gln Asn Glu Leu Ser Leu Asp Asp
 485 490 495
 Thr Thr Asp Gln His Thr Leu Asp Asn Leu Glu Lys Glu Leu Gln Val
 500 505 510
 Leu Arg Ser Leu Ala Asp Thr Ser Glu Lys Leu Tyr Ser Leu Thr Ser
 515 520 525
 Glu Glu Phe Pro Asp Phe Ser Ser Gln Ser Leu Asn Ile Ser Gln Ile
 530 535 540
 Ser Thr Asp Phe Leu Lys Thr Ser His Val Arg Gly Pro Cys Gly Val
 545 550 555 560
 Glu Glu Leu Ser Cys Ser Gly Arg Asp Thr Lys Ile Gln Ser Leu Leu
 565 570 575
 Ser Leu Ser Glu Ser Ser Thr Asp Glu Glu Glu Glu Asp Phe Leu Asn
 580 585 590
 Lys Gln His Val Ile Thr Leu Pro Trp Ser Lys Ser Thr
 595 600 605

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTCCTGGATG GCGGAGCCTT GGGTTCCGGG GGCCTGGGAC CTGCAACTCT TTCTACAAGA 60

TATCAAGTTA TTCTAGTACA ACCATATAAA TAAATAATAC CTGAAGTCTC AGTGTAACAT 120

GGACAATTAA CAGTGATGAC AGATAAATAC AGACGCATGG GGATCAAATA CTAGGCCAAAA 180

CGCTTTTTTAA AAGTGTATCA GGCTTTTAAAG AAACACTGCA GGATCCTGTC TATCTTAATG 240

CTGATAGAGC TCAGCTAAAA ATTTAGGAGG TTCTAGTATT CTTTCATGGCT GAAGCTGAGA 300

GAGTCTGAAA CCCTGATGCT TAAGCTCCAT TCTAGATCAT AGCTCCAACCT CCTTCAGGAT 360

ATAAGGAAAA GAGATTATAT TTCCACAATG ATAGATCTTT GGTGTGTACAG GTTTCCCAAT 420

GAGTGGATCA TGATGACCGT ATTGTAGGGA CTTGCCATAG TATGGCTGCT TCCCGATCTA 480

CTCGTGTTAC MAGATCAACA GTGGGGTTAA ACGGCTTGGA TGAATCTTTT TGTGGTAGAA 540

CTTTAAGGAA TCGTAGCATT GCGCATCCTG AAGAAATCTC TTCTAATTCT CAAGTACGAT 600

CAAGATCACC AAAGAAGAGA CCAGAGCCTG TGCCAATTCA GAAAGGAAAT AATAATGGGA 660

GAACCACTGA TTTAAACAG CAGAGTACCC GAGAATCATG GGTAAGCCCT AGGAAAAGAG 720

GACTTTCTTC TTCAGAAAAG GATAACATAG AAAGGCAGGC TATAGAAAAT TGTGAGAGAA 780

GGCAAACAGA ACCTGTTTCA CCAGTTTTAA AAAGAATTAA GCGTTGTCTT AGATCTGAAG 840

CACCAAACAG TTCAGAAGAA GATTCTCCTA TAAAATCAGA CAAGGAGTCA GTAGAACAGA 900

GGAGTACAGT AGTGGACAAT GATGCAGATT TTCAAGGGAC TAAACGAGCT TGTGATGTC 960

TTATACTGGA TGATTGTGAG AAAAGGGAAA TTAATAAGGT GAATGTCAGT GAGGAAGGGC 1020

CACTTAATTC TGCAGTAGTT GAAGAAATCA CAGGCTATTT GGCTGTCAAT GGTGTTGATG 1080

ACAGTGATTC AGCTGTTATA AACTGTGATG ACTGTCAGCC TGATGGGAAC ACTAAACAAA 1140

ATAGCATTGG TTCTATGTG TTACAGGAAA AATCAGTAGC TGAAAATGGG GATACGGATA 1200

CCCAAACCTC AATGTTTCCTT GATAGTAGGA AGGAGGACAG TTATATAGAC CATAAGGTGC 1260

CTTGACACAGA TTCACAAGTG CAGGTCAAGT TGGAGGACCA CAAAATAGTA ACTGCCTGCT 1320

TGCCTGTGGA ACATGTTAAT CAGCTGACTA CTGAGCCAGC TACAGGGCCC TTTTCTGAAA 1380

CTCAGTCATC TTTAAGGGAT TCTGAGGAGG AAGTAGATGT GGTGGGAGAT AGCAGTGCCT 1440

CAAAAGAGCA GTGTAAAGAA AACACCAATA ACGAAGTGA CACAAGTCTT GAGAGTATGC 1500

CAGCCTCCGG AGAACCTGAA CCATCTCCTG TTCTAGACTG TGTATCAGCT CAAATGATGT 1560

CTTTATCAGA ACCTCAAGAA CATCGTTATA CTCTGAGAAC CTCACCACGA AGGGCAGCCC 1620

CTACCAGAGG TAGTCCCCTT AAAAACAGTT CTCCTTACAG AGAAAATGGA CAATTTGAGG 1680

AGAATAATCT TAGTCCTAAT GAAACAAATG CAACTGTTAG TGATAATGTA AGTCAATCTC 1740

CTACAAATCC TGGTGAAATT TCTCAAAATG AAAAAGGGAT ATGTTGTGAC TCTCAAAATA 1800

ATGGAAGTGA AGGAGTAAGT AAACCACCCT CAGAGGCAAG ACTCAATATT GGACATTTGC 1860

CATCTGCCAA AGAGAGTGCC AGTCAGCACA TTACAGAAGA GGAAGATCAT GATCCTGATG 1920

TTTATTACTT TGAATCAGAT CATGTGGCAC TGAAACACAA CAAAGATTAT CAGAGACTAT 1980

TACAGACGAT TGCTGTACTC GAGGCTCAGC GTTCTCAAGC AGTCCAAGAC CTTGAAAGTT 2040

TAGGCAGGCA CCAGAGAGAA GCACTGAAAA ATCCCATTGG ATTTGTGGAA AAACCTCAGA 2100

AGAAGGCTGA TATTGGGCTT CCATATCCAC AGAGAGTTGT TCAATTGCCT GAGATCGTAT 2160

GGGACCAATA TACCCATAGC CTTGGGAATT TTGAAAGAGA ATTTAAAAAT CGTAAAAGAC 2220

ATACTAGAAG AGTTAAGCTA GTTTTTGATA AAGTAGGTTT ACCTGCTAGA CCAAAAAGTC 2280

CTTTAGATCC TAAGAAGGAT GGAGAGTCCC TTTCATATTC TATGTTGCCT TTGAGTGATG 2340

GTCCAGAAGG CTCAAGCAGT CGTCCTCAGA TGATAAGAGG ACGCTTGCTG GATGATACCA 2400

AACCTGAAAC ATTTAACCAG TTGTGGACTG TTGAAGAACA GAAAAAGCTG GAACAGCTAC 2460

TCATCAAATA CCCTCCTGAA GAAGTAGAAT CTCGACGCTG GCAGAAGATA GCAGATGAAT 2520

TGGGCAACAG GACAGCAAAA CAGGTTGCCA GCCGAGTACA GAAGTATTTT ATAAAGCTAA 2580

CTAAAAGCTGG CATTCAGTA CCAGGCAGAA CACCAAACTT ATATATATAC TCCAAAAGT 2640

CTTCAACAAG CAGACGACAG CACCCTCTTA ATAAGCATCT CTTTAAGCCT TCCACTTTCA 2700

TGACTTCACA TGAACCGCCA GTGTATATGG ATGAAGATGA TGACCGATCT TGTTTTCATA 2760

GCCACATGAA CACTGCTGTT GAAGATGCAT CAGATGACGA AAGTATTCCT ATCATGTATA 2820

GGAATTTACC TGAATATAAA GAACTATTAC AGTTTAAAAA GTTAAAGAAG CAGAACTTC 2880

AGCAAATGCA AGCTGAAAGT GGATTTGTGC AACATGTGGG CTTTAAGTGT GATAACTGTG 2940

GCATAGAACC CATCCAGGGT GTTCGGTGGC ATTGCCAGGA TTGTCTCCA GAAATGTCTT 3000

TGGATTTCTG TGATTCTTGT TCAGACTGTC TACATGAAAC AGATATTCAC AAGGAAGATC 3060

ACCAATTAGA ACCTATTTAT AGGTCAGAGA CATCTTAGA CAGAGACTAC TGTGTGTCTC 3120

AGGGCACCAG TTACAATTAC CTTGACCCAA ACTACTTTCC AGCAACAGA TGACATGGAA 3180

GAGAACATCA TTTACTAGTC CTCTTCAACA CATAGCAATG GTATCATTTG TAATTATGTG 3240

CACAGTTTGG AAAGATTCTC TGCTTTCCCA GAAATGACAC TCACAGCATG AGAGCTTCCT 3300

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GAGTGTTCCTC GTCAAGTACA GCTCTGCACC GTTGTGGCTC TAGATCACTG TTCAGCAGCT 3360
GAACATTCCTT GGTGAGCAAA GGTTCCTCTG GTGAATTTTT CACCACTGCG TTTTAGGTGG 3420
TGATCTTAAA TGGGTGAGAT GGAACGAGAG CACACATTAA AGAGAGAGTA AATTCCAAAG 3480
GTTTCAAAGA ACTTGGTCAT AAATATGATA ATGAGAAGAC AAAGTATTTA TATTTAAACA 3540
GTTTAGTAGC CTTTCAGTTT GTGAAAATAG TTTTCAGCAC AGAAACTGAC TTCTTTAGAC 3600
AAAGTTTTTA CCAATGATGG TGTTTGCTTC TAGGATATAC ACTTTAAAAG AACTCACTGT 3660
CCCAGTGGTG GTCATTGATG GCCTTTAGTA AATTGGAGCT GCTTAATCAT ATTGATATCT 3720
AATTTCTTTT AACCACAATG AATTGTCCTT AATTACCAAC AGTGAAGCAC TACAGGAGGC 3780
AACTGTGGCA TTGCTTCCTT AACCAGCTCA TGGTGTGTGA ATGTTATAAA ATTGTCACTC 3840
AGATATATTT TTTAAATGTA ATGTTATATA AGATGATCAT GTGATGTGTA CAAACTATGG 3900
TGAAAAGTGC CAGTGGTAGT AACTGTGTAA AGTTTCTAAT TCACAACATT AATTCCTTTA 3960
AAATACACAG CCTTCTGCCT CTGTATTTGG AGTTGTCAGT ACAACTCATC AAAGAAAAC 4020
GCCTAATATA AAAATCATAT ATATGGTAAT AATTTCCCTC TTTTGTAGTC TGCACAAGAT 4080
CCATAAAGA TTGTATTTTT ATTACTATTT AAACAAGTGA TTAAATTTAG TCTGCACAGT 4140

GAGCAAGGGT TCACATGCAT TCTTTTATAC TGCTGGATTT TGTGTGTCAT CATTTAAAAC 4200
ATTTTGTATG TTTCTTCTTA TCTGTGTATA CAGTATGTTC TTGAATGATG TTCATTTGTC 4260
AGGAGAACTG TGAGAAATAA ACTATGTGGA TACTGTCTGT TTMTRTCAA AAAAAAAAAA 4320
AAAAAAAAA AAAAAAA 4337

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(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Met Ala Ala Ser Arg Ser Thr Arg Val Thr Arg Ser Thr Val Gly Leu
 1             5             10             15

Asn Gly Leu Asp Glu Ser Phe Cys Gly Arg Thr Leu Arg Asn Arg Ser
      20             25             30

Ile Ala His Pro Glu Glu Ile Ser Ser Asn Ser Gln Val Arg Ser Arg
      35             40             45

Ser Pro Lys Lys Arg Pro Glu Pro Val Pro Ile Gln Lys Gly Asn Asn
      50             55             60

Asn Gly Arg Thr Thr Asp Leu Lys Gln Gln Ser Thr Arg Glu Ser Trp
      65             70             75             80

Val Ser Pro Arg Lys Arg Gly Leu Ser Ser Ser Glu Lys Asp Asn Ile
      85             90             95

Glu Arg Gln Ala Ile Glu Asn Cys Glu Arg Arg Gln Thr Glu Pro Val
      100            105            110

Ser Pro Val Leu Lys Arg Ile Lys Arg Cys Leu Arg Ser Glu Ala Pro
      115            120            125

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Asn Ser Ser Glu Glu Asp Ser Pro Ile Lys Ser Asp Lys Glu Ser Val																			
130						135					140								
Glu Gln Arg Ser Thr Val Val Asp Asn Asp Ala Asp Phe Gln Gly Thr																			
145					150					155									160
Lys Arg Ala Cys Arg Cys Leu Ile Leu Asp Asp Cys Glu Lys Arg Glu																			
				165					170										175
Ile Lys Lys Val Asn Val Ser Glu Glu Gly Pro Leu Asn Ser Ala Val																			
			180						185										190
Val Glu Glu Ile Thr Gly Tyr Leu Ala Val Asn Gly Val Asp Asp Ser																			
			195					200						205					
Asp Ser Ala Val Ile Asn Cys Asp Asp Cys Gln Pro Asp Gly Asn Thr																			
			210				215						220						
Lys Gln Asn Ser Ile Gly Ser Tyr Val Leu Gln Glu Lys Ser Val Ala																			
225						230					235								240
Glu Asn Gly Asp Thr Asp Thr Gln Thr Ser Met Phe Leu Asp Ser Arg																			
				245					250										255
Lys Glu Asp Ser Tyr Ile Asp His Lys Val Pro Cys Thr Asp Ser Gln																			
			260					265											270
Val Gln Val Lys Leu Glu Asp His Lys Ile Val Thr Ala Cys Leu Pro																			
			275				280												285
Val Glu His Val Asn Gln Leu Thr Thr Glu Pro Ala Thr Gly Pro Phe																			
			290				295						300						
Ser Glu Thr Gln Ser Ser Leu Arg Asp Ser Glu Glu Glu Val Asp Val																			
305						310					315								320
Val Gly Asp Ser Ser Ala Ser Lys Glu Gln Cys Lys Glu Asn Thr Asn																			
						325				330									335
Asn Glu Leu Asp Thr Ser Leu Glu Ser Met Pro Ala Ser Gly Glu Pro																			
			340					345											350
Glu Pro Ser Pro Val Leu Asp Cys Val Ser Ala Gln Met Met Ser Leu																			
			355				360							365					
Ser Glu Pro Gln Glu His Arg Tyr Thr Leu Arg Thr Ser Pro Arg Arg																			
			370				375							380					
Ala Ala Pro Thr Arg Gly Ser Pro Thr Lys Asn Ser Ser Pro Tyr Arg																			
385						390					395								400
Glu Asn Gly Gln Phe Glu Glu Asn Asn Leu Ser Pro Asn Glu Thr Asn																			
				405						410									415
Ala Thr Val Ser Asp Asn Val Ser Gln Ser Pro Thr Asn Pro Gly Glu																			
			420					425											430

Ile Ser Gln Asn Glu Lys Gly Ile Cys Cys Asp Ser Gln Asn Asn Gly
 435 440 445
 Ser Glu Gly Val Ser Lys Pro Pro Ser Glu Ala Arg Leu Asn Ile Gly
 450 455 460
 His Leu Pro Ser Ala Lys Glu Ser Ala Ser Gln His Ile Thr Glu Glu
 465 470 475 480
 Glu Asp Asp Asp Pro Asp Val Tyr Tyr Phe Glu Ser Asp His Val Ala
 485 490 495
 Leu Lys His Asn Lys Asp Tyr Gln Arg Leu Leu Gln Thr Ile Ala Val
 500 505 510
 Leu Glu Ala Gln Arg Ser Gln Ala Val Gln Asp Leu Glu Ser Leu Gly
 515 520 525
 Arg His Gln Arg Glu Ala Leu Lys Asn Pro Ile Gly Phe Val Glu Lys
 530 535 540
 Leu Gln Lys Lys Ala Asp Ile Gly Leu Pro Tyr Pro Gln Arg Val Val
 545 550 555 560
 Gln Leu Pro Glu Ile Val Trp Asp Gln Tyr Thr His Ser Leu Gly Asn
 565 570 575
 Phe Glu Arg Glu Phe Lys Asn Arg Lys Arg His Thr Arg Arg Val Lys
 580 585 590
 Leu Val Phe Asp Lys Val Gly Leu Pro Ala Arg Pro Lys Ser Pro Leu
 595 600 605
 Asp Pro Lys Lys Asp Gly Glu Ser Leu Ser Tyr Ser Met Leu Pro Leu
 610 615 620
 Ser Asp Gly Pro Glu Gly Ser Ser Ser Arg Pro Gln Met Ile Arg Gly
 625 630 635 640
 Arg Leu Cys Asp Asp Thr Lys Pro Glu Thr Phe Asn Gln Leu Trp Thr
 645 650 655
 Val Glu Glu Gln Lys Lys Leu Glu Gln Leu Leu Ile Lys Tyr Pro Pro
 660 665 670
 Glu Glu Val Glu Ser Arg Arg Trp Gln Lys Ile Ala Asp Glu Leu Gly
 675 680 685
 Asn Arg Thr Ala Lys Gln Val Ala Ser Arg Val Gln Lys Tyr Phe Ile
 690 695 700
 Lys Leu Thr Lys Ala Gly Ile Pro Val Pro Gly Arg Thr Pro Asn Leu
 705 710 715 720
 Tyr Ile Tyr Ser Lys Lys Ser Ser Thr Ser Arg Arg Gln His Pro Leu
 725 730 735

Asn Lys His Leu Phe Lys Pro Ser Thr Phe Met Thr Ser His Glu Pro
 740 745 750
 Pro Val Tyr Met Asp Glu Asp Asp Arg Ser Cys Phe His Ser His
 755 760 765
 Met Asn Thr Ala Val Glu Asp Ala Ser Asp Asp Glu Ser Ile Pro Ile
 770 775 780
 Met Tyr Arg Asn Leu Pro Glu Tyr Lys Glu Leu Leu Gln Phe Lys Lys
 785 790 795 800
 Leu Lys Lys Gln Lys Leu Gln Gln Met Gln Ala Glu Ser Gly Phe Val
 805 810 815
 Gln His Val Gly Phe Lys Cys Asp Asn Cys Gly Ile Glu Pro Ile Gln
 820 825 830
 Gly Val Arg Trp His Cys Gln Asp Cys Pro Pro Glu Met Ser Leu Asp
 835 840 845
 Phe Cys Asp Ser Cys Ser Asp Cys Leu His Glu Thr Asp Ile His Lys
 850 855 860
 Glu Asp His Gln Leu Glu Pro Ile Tyr Arg Ser Glu Thr Phe Leu Asp
 865 870 875 880
 Arg Asp Tyr Cys Val Ser Gln Gly Thr Ser Tyr Asn Tyr Leu Asp Pro
 885 890 895
 Asn Tyr Phe Pro Ala Asn Arg
 900

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AATCGGGACC CCATCCCCCA AATCACTGGA TCCTGCAGCC CCACATCCTA AGGTGGATCC 60
 CACGCTTCCC TGTGCCCCCT ACTGGATCCT GGACCTCTAC GTCTTAACCA CTGGATCCCCA 120
 CACAAATCAG TGAATGGATC CCAACACCCC AACCACAGGA GCACGGATTC CCTGTACCTC 180
 AACACCCAGA CCCTGCCTCC CTCAGGCACC AGATCCAGTG TCCTAGTGAA ACGCTGGATC 240
 CTAGATCCCC AACCCCAGAT CCCCATGCCT CGAGCCCTGG ATCTCCAAGC TCAGCTGCTG 300
 GATTCTGGAT GTCAACAAAC CTCACCACTG GATCCTGACA ACCACAATGC CTGGATCCTG 360
 GGGCCCCCAT CACTGGATCC CAGATCCCCT CACTCCACCC ACTGGATTCC TGCATTGGTT 420

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TTTGGTTTTT TGTTTTTTTT TTAACCTCGA CACTGGGTCT CAGATCCTTC TGCTGACTGC 480
CAGATCCCTG CATTTC AAGC ACTACGCCCT CCACCCCCAG GCACTGGATC CCAGATTCCC 540
AAGCCTTCAC CCACCAGATT CTGGCTCCTA AAACAAGTGC GGGGGCCCCA GTGGCACAGC 600
AAGTGGATCC TGGCAACTGC AGCTGCTGGA TTCCAGATTC TGGGTCCCCA ATCCCTCTGC 660
CCAGTCCCTC AATGTTGAAA CCTCATCTCT TGAAGGCAGA TCCTGATATT CCAAGGCACT 720
GAATCCCAAG CCCTGAATCC CCGGTTTCTG ATCTGAATCT TCCAGGCGCC GGGTCCCAA 780
TGTTTCAGGCC CCAAGTCTAG ATCCTGGCAG CCCAGTCACA GAGTATCCCA CACACACTGG 840
TGCCCAGAGC CGGCTTCTCA TGACATGAAA TTGCATGGTC GAGGGAGTCT GTGGGGAAGG 900
AAGCCCAGGT CCTGGCTGCA ACCTGCACGG ATGCTGGATT CCCCCTCACC CCACCTCTGC 960
ATGGCCACCC CCTCCAGCC CTGTGGGGAA ACTGTTCCCT GGAACCACTC CACTCCCTGC 1020
ATCCCCACAC TTCACAGCAT CTTCCATCCC CCTCCCCTT CTAGGCGAAT AGTCCCCAGA 1080
GCTGTGTTCC TCCAAGGGGT CCGAGGAATC ACTCACTCCT GGAGGCTGGC AAGGAGACAG 1140
TCTGAGGCCA GGGACACATG AAGGGATGTC CCCACCCAG CACTATCAGG GCCTCCCCAG 1200
GCTTCCAGAG TTGAAAGCCA GGAGAAAATC GGCAAAGACC ACCCTTCCCT AAACCCAAGC 1260
ACCCAATGAT GCRAAAAAAA AAAAAAAAAA AAAAAAAAAA 1299

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(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

Met Lys Leu His Gly Arg Gly Ser Leu Trp Gly Arg Lys Pro Arg Ser
 1                5                10                15
Trp Leu Gln Pro Ala Arg Met Leu Asp Ser Pro Ser Pro His Leu Cys
                20                25                30
Met Ala Thr Pro Ser Gln Pro Cys Gly Glu Thr Val Pro Trp Asn His
                35                40                45
Ser Thr Pro Cys Ile Pro Thr Leu His Ser Ile Phe His Pro Pro Pro
                50                55                60
Thr Ser Arg Arg Ile Val Pro Arg Ala Val Phe Leu Gln Gly Val Arg
        65                70                75                80
Gly Ile Thr His Ser Trp Arg Leu Ala Arg Arg Gln Ser Glu Ala Arg
                85                90                95
Asp Thr

```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

CTCCTCTGTC CACTGCTTTC GTGAAGACAA GATGAAGTTC ACAATTGTCT TTGCTGGACT 60
TCTTGGAGTC TTTCTAGCTC CTGCCCTAGC TAACTATAAT ATCAACGTCA ATGATGACAA 120
CAACAATGCT GGAAGTGGGC AGCAGTCAGT GAGTGTCAAC AATGAACACA ATGTGGCCAA 180
TGTTGACAAT AACACGGAT GGGACTCCTG GAATTCCATC TGGGATTATG GAAATGGCTT 240
TGCTGCAACC AGACTCTTTC AAAAGAAGAC ATGCATTGTG CACAAAATGA ACAAGGAAGT 300
CATGCCCTCC ATTCAATCCC TTGATGCACT GGTCAAGGAA AAGAAGCTTC AGGGTAAGGG 360
ACCAGGAGGA CCACCTCCCA AGGGCCTGAT GTACTCAGTC AACCCAAACA AAGTCGATGA 420
CCTGAGCAAG TTCGGAAAAA ACATTGCAAA CATGTGTCGT GGGATTCCAA CATACATGGC 480
TGAGGAGATG CAAGAGGCAA GCCTGTTTTT TTACTCAGGA ACGTGCTACA CGACCAAGTGT 540
ACTATGGATT GTGGACATTT CTTTCTGTGG AGACACGGTG GAGAACTAAA CAATTTTTTA 600
AAGCCACTAT GGATTTAGTC ATCTGAATAT GCTGTGCAGA AAAAATATGG GCTCCAGTGG 660
TTTTTACCAT GTCATTCTGA AATTTTCTC TACTAGTTAT GTTTGATTTC TTTAAGTTTC 720
AATAAAATCA TTTAGCCTTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 780
AAAAAAAAA A                                     791

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(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu Ala
 1             5             10             15
Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn Asn Asn
          20             25             30
Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu His Asn Val
          35             40             45
Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp Asn Ser Ile Trp
          50             55             60
Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu Phe Gln Lys Lys Thr
          65             70             75             80
Cys Ile Val His Lys Met Asn Lys Glu Val Met Pro Ser Ile Gln Ser
          85             90             95
Leu Asp Ala Leu Val Lys Glu Lys Lys Leu Gln Gly Lys Gly Pro Gly
          100             105             110

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Gly Pro Pro Pro Lys Gly Leu Met Tyr Ser Val Asn Pro Asn Lys Val
115 120 125

Asp Asp Leu Ser Lys Phe Gly Lys Asn Ile Ala Asn Met Cys Arg Gly
130 135 140

Ile Pro Thr Tyr Met Ala Glu Glu Met Gln Glu Ala Ser Leu Phe Phe
145 150 155 160

Tyr Ser Gly Thr Cys Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile
165 170 175

Ser Phe Cys Gly Asp Thr Val Glu Asn
180 185

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2012 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTCAAGTTCA TCATTGTCCT GAGAGAGAGG AGCAGCGCGG TTCTCGGCCG GGACAGCAGA 60
ACGCCAGGGG ACCCTCACCT GGGCGCGCCG GGGCACGGGC TTTGATTGTC CTGGGGTTCGC 120
GGAGACCCGC GCGCCTGCCC TGCACGCCGG GCGGCAACCT TTGCAGTCGC GTTGGCTGCT 180
GCGATCGGCC GCGGGGTCCC TGCCGAAGGC TCGGCTGCTT CTGTCCACCT CTTACACTTC 240
TTCATTTATC GGTGGATCAT TTCGAGAGTC CGTCTTGTA ATGTTTGGCA CTTTGCTACT 300
TTATTGCTTC TTTCTGGCGA CAGTTCCAGC ACTCGCCGAG ACCGGCGGAG AAAGGCAGCT 360
GAGCCCGGAG AAGAGCGAAA TATGGGGACC CGGGCTAAAA GCAGACGTCG TCCTTCCCGC 420
CCGCTATTTT TATATTCAGG CAGTGGATAC ATCAGGGAAT AAATTCACAT CTTCTCCAGG 480
CGAAAAGGTC TTCCAGGTGA AAGTCTCAGC ACCAGAGGAG CAATTCACCTA GAGTTGGAGT 540
CCAGGTTTTA GACCGAAAAG ATGGGTCTCT CATAGTAAGA TACAGAATGT ATGCAAGCTA 600
CAAAAATCTG AAGGTGGAAA TTAAATTCCA AGGGCAACAT GTGGCCAAAT CCCCATATAT 660
TTTAAAAGGG CCGGTTTACC ATGAGAACTG TGA CTGTCTCT CTGCAAGATA GTGCAGCCTG 720
GCTACGGGAG ATGAACTGCC CTGAAACCAT TGCTCAGATT CAGAGAGATC TGGCACATTT 780
CCCTGCTGTG GATCCAGAAA AGATTGCAGT AGAAATCCCA AAAAGATTG GACAGAGGCA 840
GAGCCTATGT CACTACACCT TAAAGGATA CAAGGTTTAT ATCAAGACTC ATGGTGAACA 900
TG TAGGTTTT AGAATTTTCA TGGATGCCAT ACTACTTTCT TTGACTAGAA AGGTGAAGAT 960
GCCAGATGTG GAGCTCTTTG TTAATTTGGG AGACTGGCCT TTGGAAAAAA AGAAATCCAA 1020
TTCAAACATC CATCCGATCT TTTCTGTTG TGGCTCCACA GATTCCAAGG ATATCGTGAT 1080
GCCTACGTAC GATTTGACTG ATTCTGTTCT GGAAACCATG GGCCGGGTAA GTCTGGATAT 1140
GATGTCCGTG CAAGCTAACA CGGGTCCTCC CTGGGAAAGC AAAAATTCCA CTGCCGTCTG 1200
GAGAGGGCGA GACAGCCGCA AAGAGAGACT CGAGCTGGTT AAATCAGTA GAAAACACCC 1260
AGAACTCATA GACGCTGCTT TCACCAACTT TTTCTTCTTT AAACAGGATG AAAACCTGTA 1320
TGGTCCCATT GTGAAACATA TTTCATTTTT TGATTCTTTC AAGCATAAGT ATCAAATAAA 1380
TATCGATGGC ACTGTAGCAG CTTATCGCCT GCCATATTTG CTAGTTGGTG ACAGTGTGTG 1440
GCTGAAGCAG GATTCCATCT ACTATGAACA TTTTACAAAT GAGCTGCAGC CCTGGAAACA 1500
CTACATTCCA GTTAAGAGCA ACCTGAGCGA TCTGCTAGAA AAATTTAAAT GGGCGAAAGA 1560
TCACGATGAA GAGGCCAAAA AGATAGCAAA AGCAGGACAA GAATTTGCAA GAAATAATCT 1620
CATGGGCGAT GACATATTCT GTTATTATTT CAACTYTTT CAGGAATATG CCAATTTACA 1680

AGTGAGTGAG CCCCAAATCC GAGAGGGGCAT GAMAAGGGTA GAACCACAGA CTGAGGACGA 1740
 CCTCTTCCST TGTACTTGCC ATAGGAAAAA GACCAAAGAT GAACTSTGAT ATGCAAAATA 1800
 ACTTCTATTA GAATAATGGT GCTCTGAAGA CTCTTCTTAA CTAAAAAGAA GAATTTTTTTT 1860
 AAGTATTAAT TCCATGGACA ATATAAAATC TGTGTGATTG TTTGCAGTAT GAAGACACAT 1920
 TTCTACTTAT GCAGTATTCT CATGACTGTA CTTTAAAGTA CATTTTATAA ATTTTATAAT 1980
 AAAACCACCT TTATTTTAAA AAAAAAAAAA AA 2012

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	Phe	Gly	Thr	Leu	Leu	Leu	Tyr	Cys	Phe	Phe	Leu	Ala	Thr	Val	Pro	1	5	10	15
Ala	Leu	Ala	Glu	Thr	Gly	Gly	Glu	Arg	Gln	Leu	Ser	Pro	Glu	Lys	Ser	20	25	30	
Glu	Ile	Trp	Gly	Pro	Gly	Leu	Lys	Ala	Asp	Val	Val	Leu	Pro	Ala	Arg	35	40	45	
Tyr	Phe	Tyr	Ile	Gln	Ala	Val	Asp	Thr	Ser	Gly	Asn	Lys	Phe	Thr	Ser	50	55	60	
Ser	Pro	Gly	Glu	Lys	Val	Phe	Gln	Val	Lys	Val	Ser	Ala	Pro	Glu	Glu	65	70	75	80
Gln	Phe	Thr	Arg	Val	Gly	Val	Gln	Val	Leu	Asp	Arg	Lys	Asp	Gly	Ser	85	90	95	
Phe	Ile	Val	Arg	Tyr	Arg	Met	Tyr	Ala	Ser	Tyr	Lys	Asn	Leu	Lys	Val	100	105	110	
Glu	Ile	Lys	Phe	Gln	Gly	Gln	His	Val	Ala	Lys	Ser	Pro	Tyr	Ile	Leu	115	120	125	
Lys	Gly	Pro	Val	Tyr	His	Glu	Asn	Cys	Asp	Cys	Pro	Leu	Gln	Asp	Ser	130	135	140	
Ala	Ala	Trp	Leu	Arg	Glu	Met	Asn	Cys	Pro	Glu	Thr	Ile	Ala	Gln	Ile	145	150	155	160
Gln	Arg	Asp	Leu	Ala	His	Phe	Pro	Ala	Val	Asp	Pro	Glu	Lys	Ile	Ala	165	170	175	
Val	Glu	Ile	Pro	Lys	Arg	Phe	Gly	Gln	Arg	Gln	Ser	Leu	Cys	His	Tyr	180	185	190	
Thr	Leu	Lys	Asp	Asn	Lys	Val	Tyr	Ile	Lys	Thr	His	Gly	Glu	His	Val				

195	200	205
Gly Phe Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys 210 215 220		
Val Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro 225 230 235 240		
Leu Glu Lys Lys Lys Ser Asn Ser Asn Ile His Pro Ile Phe Ser Trp 245 250 255		
Cys Gly Ser Thr Asp Ser Lys Asp Ile Val Met Pro Thr Tyr Asp Leu 260 265 270		
Thr Asp Ser Val Leu Glu Thr Met Gly Arg Val Ser Leu Asp Met Met 275 280 285		
Ser Val Gln Ala Asn Thr Gly Pro Pro Trp Glu Ser Lys Asn Ser Thr 290 295 300		
Ala Val Trp Arg Gly Arg Asp Ser Arg Lys Glu Arg Leu Glu Leu Val 305 310 315 320		
Lys Leu Ser Arg Lys His Pro Glu Leu Ile Asp Ala Ala Phe Thr Asn 325 330 335		
Phe Phe Phe Phe Lys Gln Asp Glu Asn Leu Tyr Gly Pro Ile Val Lys 340 345 350		
His Ile Ser Phe Phe Asp Phe Phe Lys His Lys Tyr Gln Ile Asn Ile 355 360 365		
Asp Gly Thr Val Ala Ala Tyr Arg Leu Pro Tyr Leu Leu Val Gly Asp 370 375 380		
Ser Val Val Leu Lys Gln Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn 385 390 395 400		
Glu Leu Gln Pro Trp Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser 405 410 415		
Asp Leu Leu Glu Lys Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala 420 425 430		
Lys Lys Ile Ala Lys Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met 435 440 445		
Gly Asp Asp Ile Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala 450 455 460		
Asn Leu Gln Val Ser Glu Pro Gln Ile Arg Glu Gly Met Xaa Arg Val 465 470 475 480		
Glu Pro Gln Thr Glu Asp Asp Leu Phe Xaa Cys Thr Cys His Arg Lys 485 490 495		
Lys Thr Lys Asp Glu Leu		

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GNAAGAAGAG AGCAACAGCC AGGACCAAG

29

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CNCAGGCTAG GCACTGATTC TGCTGGTTC

29

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GNAGACATGA AAGTTGAGCA GAAGGAAAG

29

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GNGGTGCTTT TGATATCCAG CCATCTCTA

29

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNTGGAAAGA GGAGCAAGAA CCAAGGCAG

29

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TNGGTTTTGT ACGTTGTGCT CTTTTCATC

29

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TNATGGTCTA TATAACTGTC CTCCTTCCT

29

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CNACACTGGG TCTCAGATCC TTCTGCTGA

29

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GNCTCCAAGA AGTCCAGCAA AGACAATTG

29

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ANTGCCAAAC ATTTACAAGA CGGACTCTC

29

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1776 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

AGCTCACAGT AGCCCGGCGG CCCAGGGCAA TCCGACCACA TTTCACCTCTC ACCGCTGTAG 60

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GAATCCAGAT GCAGGCCAAG TACAGCAGCA CGAGGGACAT GCTGGATGAT GATGGGGACA 120
CCACCATGAG CCTGCATTCT CAAGCCTCTG CCACAACCTCG GCATCCAGAG CCCCAGCGCA 180
CAGAGCACAG GGCTCCCTCT TCAACGTGGC GACCAGTGGC CCTGACCCTG CTGACTTTGT 240
GCTTGGTGCT GCTGATAGGG CTGGCAGCCC TGGGGCTTTT GTTTTTTCAG TACTACCAGC 300
TCTCCAATAC TGGTCAAGAC ACCATTTCTC AAATGGAAGA AAGATTAGGA AATACGTCCC 360
AAGAGTTGCA ATCTCTTCAA GTCCAGAATA TAAAGCTTGC AGGAAGTCTG CAGCATGTGG 420
CTGAAAAACT CTGTCGTGAG CTGTATAACA AAGCTGGAGC ACACAGGTGC AGCCCTTGTA 480
CAGAACAATG GAAATGGCAT GGAGACAATT GCTACCAGTT CTATAAAGAC AGCAAAAGTT 540
GGGAGGACTG TAAATATTTT TGCCTTAGTG AAAACTCTAC CATGCTGAAG ATAAACAAAC 600
AAGAAGACCT GGAATTTGCC GCGTCTCAGA GCTACTCTGA GTTTTCTAC TCTTATTGGA 660
CAGGGCTTTT GCGCCCTGAC AGTGGCAAGG CCTGGCTGTG GATGGATGGA ACCCCTTTCA 720
CTTCTGAAC TTTCCATATT ATAATAGATG TCACCAGCCC AAGAAGCAGA GACTGTGTGT 780
CCATCCTTAA TGGGATGATC TTCTCAAAGA ACTGCAAAGA ATTGAAGCGT TGTGTCTGTG 840
AGAGAAGGCG AGGAATGGTG AAGCCAGAGA GCCTCCATGT CCCCCTGAA ACATTAGGCG 900
AAGGTGACTG ATTCGCCCTC TGCAACTACA AATAGCAGAG TGAGCCAGGC GGTGCCAAAG 960
CAAGGGCTAG TTGAGACATT GGGAAATGGA ACATAATCAG GAAAGACTAT CTCTCTGACT 1020
AGTACAAAAT GGGTTCTCGT GTTTCCTGTT CAGGATCACC AGCATTTCTG AGCTTGGGTT 1080
TATGCACGTA TTTAACAGTC ACAAGAAGTC TTATTTACAT GCCACCAACC AACCTCAGAA 1140
ACCCATAATG TCATCTGCCT TCTTGGCTTA GAGATAACTT TTAGCTCTCT TTCTTCTCAA 1200
TGTCTAATAT CACCTCCCTG TTTTCATGTC TTCCTTACAC TTGGTGGAAAT AAGAACTTT 1260
TTGAAGTAGA GGAAATACAT TGAGGTAACA TCCTTTTCTC TGACAGTCAA GTAGTCCATC 1320
AGAAATTGGC AGTCACTTCC CAGATTGTAC CAGCAAATAC ACAAGGAATT CTTTTTGTTT 1380
GTTTCAGTTC ATACTAGTCC CTTCCCAATC CATCAGTAAA GACCCCATCT GCCTTGTCCA 1440
TGCCGTTTCC CAACAGGGAT GTCACTTGAT ATGAGAATCT CAAATCTCAA TGCCTTATAA 1500
GCATTCCTTC CTGTGTCCAT TAAGACTCTG ATAATTGTCT CCCCTCCATA GGAATTTCTC 1560
CCAGGAAAGA AATATATCCC CATCTCCGTT TCATATCAGA ACTACCGTCC CCGATATTCC 1620
CTTCAGAGAG ATTAAAGACC AGAAAAAAGT GAGCCTCTTC ATCTGCACCT GTAATAGTTT 1680
CAGTTCCTAT TTTCTTCCAT TGACCCATAT TTATACCTTT CAGGTACTGA AGATTTAATA 1740
ATAATAAATG TAAATACTGT GAAAAAATAA AAAAAA 1776

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(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly
 1             5             10             15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
      20             25             30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
      35             40             45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
      50             55             60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn

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65		70		75		80
Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr						
	85			90		95
Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly						
	100		105		110	
Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys						
	115		120		125	
Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His						
	130		135		140	
Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp						
145		150		155		160
Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn						
	165		170		175	
Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe						
	180		185		190	
Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala						
	195		200		205	
Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile						
	210		215		220	
Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu						
225		230		235		240
Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val						
	245		250		255	
Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro						
	260		265		270	
Pro Glu Thr Leu Gly Glu Gly Asp						
	275		280			

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CAACTATCCC ATAATTATT TATTCTTCTT CAATGTTTGT AAAGTGCATG AGTCATGTTC 60

A C A C T T G A A G T C T A G T A G T G C A C T G T A A T A A T T C A T T T T T T A A A A G A T T A T T T A A T G C C C 120
 A T T T C A A A A T A C A G T A G T T T A C A C A G C T A C A G A A C A A T T T G G G G C A A G T T T T A A A A C A C 180
 T G A A A C A G T A A T A G T T A T T G T G T C A C A T A A A C T G A T T T G T T T T T A C A G C C A A A C C T C 240
 T G T C A G T C A G A G G C A T T C A T T A G T T T T A T A C A T G T A A T T T G A A A A T C A C T A A A C C T C G T T 300
 T T C T C A G C A G C A A T A A T T T A A G A G G C T T C A A A A T A T A A T T T C A C T C T T A T T T A G T A T T T 360
 T T T C C T G G G G G G A T T T T T A C G T A A T T T T T T A T G A A A A G A C A A A T G C A T G T T G A G A T A A C 420
 T T C T G G G A T T A A A A T A G T C T T T T G C T T T A C T T T T T T G G T T T C C T A A A A C A A C T T T A T T G A 480
 C T T T T A G T C C A T A C T G T T A T A T T T T T G T C T T A A A G A A A A T T T A A A C T A C A A A T A C C A A A A 540
 G A A A C A T T T T A A A T T T A G G G A T G A G A C T T T G G T G T A T C G T G G G T C T A G G T T T A A T G A A C 600
 A C A T C T G G G G T T A A G T T G G C A T T T C T T C A C A T C T C C A C A C C C A C A C C A A C C A T C A C A G C C 660
 C C C C A C C A A C C T T C T C C C A A C C C C A A A A G C A T T G T C C A G G G A T A T A G A T T T T A C C A A A G G 720
 C T T C T G G G A A G A C G A G G G A G C A A C A C T T T A G A T T A A A T G T G A T C A G A C T T T C C T A T T A G 780
 A T A T G G C T C T T C T G T C T C T T G T T A T C C C C C T G A C A G C T C T G C C A T A A A G T C C C T T C T C C T 840
 C A T C C T T C C C A A A C A G G C T G T A T A A G T G C T T T G A G G T A A T T A A A C T C T T T C C T C C A G T T T 900
 A C A A A T A T C A C T T A A C A 947

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met	Arg	Leu	Trp	Cys	Ile	Val	Gly	Leu	Gly	Leu	Met	Asn	Thr	Ser	Gly
1				5					10					15	
Val	Lys	Leu	Ala	Phe	Leu	His	Ile	Ser	Thr	Pro	Thr	Pro	Thr	Ile	Thr
			20					25					30		
Ala	Pro	His	Gln	Pro	Ser	Pro	Asn	Pro	Lys	Ser	Ile	Val	Gln	Gly	Tyr
		35					40					45			
Arg	Phe	Tyr	Gln	Arg	Leu	Pro	Gly	Lys	Thr	Arg	Glu	Gln	His	Phe	Arg
	50					55				60					
Leu	Asn	Val	Ile	Arg	Leu	Ser	Tyr								
65					70										

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CGCTGACTTG GGCAATGGGG CCGGTGGGGT TTGGGGGCGG AAGAGACCCT CGGGGTTGAG 60

AAGTATGTGG TGGCCTTTTCG TCCCCTGTAA AACATTGTCA CACGGTGTGG GGCGGCAGCG 120
 CTGGATCTTT GCAAGGCTAT TTTGGCATTTC TGCTGGATAT ATGTTTCGTAA ATACCAAAGT 180
 CGGCGGGAAA GTGAAGTTGT CTCCACCATA ACAGCAATTT TTTCTCTAGC AATTGCACTT 240
 ATCACATCAG CACTTCTACC AGTGGATATA TTTTTGGTTT CTTACATGAA AAATCAAAAT 300
 GGTACATTTA AGGACTGGGC TAATGCTAAT GTCAGCAGAC AGATTGAGGA CACTGTATTA 360
 TACGGTTACT ATACTTTATA TTCTGTTATA TTGTTCTGTG TGTTCTTCTG GATCCCTTTT 420
 GTCTACTTCT ATTATGAAGA AAAGGATGAT GATGATACTA GTAAATGTAC TCAAATTTAA 480
 ACGGCACTCA AGTATACTTT GGGATTTGTT GTGATTTGTG CACTGCTTCT TTTAGTTGGT 540
 GCCTTTGTTC CATTGAATGT TCCCAATAAC AAAAATTCTA CAGAGTGGGA AAAAGTGAAG 600
 TCCCTATTTG AAGAACTTGG AAGTAGTCAT GGTTTAGCTG CATTGTCATT TTCTATCAGT 660
 TCTCTGACCT TGATTGGAAT GTTGGCAGCT ATAACCTACA CAGCCTATGG CATGTCTGCG 720
 TTACCTTTAA ATCTGATAAA AGGCACTAGA AGCGCTGCTT ATGAACGTTT GGAAAACACT 780
 GAAGACATTG AAGAAGTAGA ACAACACATT CAAACGATTA AATCAAAAAG CAAAGATGGT 840
 CGACCTTTGC CAGCAAGGGA TAAACGCGCC TTAACAACAT TTGAAGAAAG GTTACGAACA 900
 CTTAAGAAGA GAGAGAGGCA TTTAGAATTC ATTGAAAACA GCTGGTGGAC AAAATTTTGT 960
 GGCGCTCTGC GTCCCCTGAA GATCGTCTGG GGAATATTTT TCATCTTAGT TGCATTGCTG 1020
 TTTGTAATTT CTCTTTTCTT GTCAAATTTA GATAAAGCTC TTCAATTCAGC TGGAATAGAT 1080
 TCTGGTTTCA TAATTTTTTG AGCTAACCTG AGTAATCCAC TGAATATGCT TTTGCCTTTA 1140
 CTACAAACAG TTTTCCCTCT TGATTATATT CTTATAACAA TTATTATTAT GTACTTTATT 1200
 TTTACTTCAA TGGCAGGAAT TCGAAATATT GGCATATGGT TCTTTTGGAT TAGATTATAT 1260
 AAAATCAGAA GAGGTAGAAC CAGGCCCCAA GCACCTCCTT TTCTCTGCAT GATACTTCTG 1320
 CTTATTGTCC TTCACACTAG CTACATGATT TATAGTCTTG CTCCCCAATA TGTTATGTAT 1380
 GGAAGCCAAA ATTACTTAAT AGAGACTAAT ATAACCTCTG ATAATCATAA AGGCAATTCA 1440
 ACCCTTTCTG TGCCAAAGAG ATGTGATGCA GATGCTCCTG AAGATCAGTG TACTGTTACC 1500
 CGGACATACC TATTCCTTCA CAAGTTCTGG TTCTTCAGTG CTGCTTACTA TTTTGGTAAC 1560
 TGGGCCTTTC TTGGGGTATT TTTGATTGGA TTAATTGTAT CCTGTTGTAA AGGGAAGAAA 1620
 TCGGTTATTG AAGGAGTAGA TGAAGATTCA GACATAAGTG ATGATGAGCC CTCTGTCTAT 1680
 TCTGCTTGAC AGCCTTCTGT CTTAAAGGTT TTATAATGCT GACTGAATAT CTGTTATGCA 1740
 TTTTTAAAGT ATTAACTAA CATTAGGATT TGCTAACTAG CTTTCATCAA AAATGGGAGC 1800
 ATGGCTATAA GACAACTATA TTTTATTATA TGTTTTCTGA AGTAACATTG TATCATAGAT 1860
 TAACATTTTA AATTACCATA ATCATGCTAT GTAAATATAA GACTACTGGC TTTGTGAGGG 1920
 AATGTTTGTG CAAAATTTTT TCCTCTAATG TATAATAGTG TTAAATTGAT TAAAAATCTT 1980
 CCAGAATTAA TATTCCTTTT TGTCACTTTT TGAAAACATA ATAAATCATT TGTATCTGTG 2040
 CCTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2100
 AAAAAAAAAA AAAAAAAAAA

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met	Lys	Asn	Gln	Asn	Gly	Thr	Phe	Lys	Asp	Trp	Ala	Asn	Ala	Asn	Val
1				5				10						15	
Ser	Arg	Gln	Ile	Glu	Asp	Thr	Val	Leu	Tyr	Gly	Tyr	Tyr	Thr	Leu	Tyr
			20					25					30		
Ser	Val	Ile	Leu	Phe	Cys	Val	Phe	Phe	Trp	Ile	Pro	Phe	Val	Tyr	Phe
			35				40					45			

Tyr Tyr Glu Glu Lys Asp Asp Asp Asp Thr Ser Lys Cys Thr Gln Ile
 50 55 60
 Lys Thr Ala Leu Lys Tyr Thr Leu Gly Phe Val Val Ile Cys Ala Leu
 65 70 75 80
 Leu Leu Leu Val Gly Ala Phe Val Pro Leu Asn Val Pro Asn Asn Lys
 85 90 95
 Asn Ser Thr Glu Trp Glu Lys Val Lys Ser Leu Phe Glu Glu Leu Gly
 100 105 110
 Ser Ser His Gly Leu Ala Ala Leu Ser Phe Ser Ile Ser Ser Leu Thr
 115 120 125
 Leu Ile Gly Met Leu Ala Ala Ile Thr Tyr Thr Ala Tyr Gly Met Ser
 130 135 140
 Ala Leu Pro Leu Asn Leu Ile Lys Gly Thr Arg Ser Ala Ala Tyr Glu
 145 150 155 160
 Arg Leu Glu Asn Thr Glu Asp Ile Glu Glu Val Glu Gln His Ile Gln
 165 170 175
 Thr Ile Lys Ser Lys Ser Lys Asp Gly Arg Pro Leu Pro Ala Arg Asp
 180 185 190
 Lys Arg Ala Leu Lys Gln Phe Glu Glu Arg Leu Arg Thr Leu Lys Lys
 195 200 205
 Arg Glu Arg His Leu Glu Phe Ile Glu Asn Ser Trp Trp Thr Lys Phe
 210 215 220
 Cys Gly Ala Leu Arg Pro Leu Lys Ile Val Trp Gly Ile Phe Phe Ile
 225 230 235 240
 Leu Val Ala Leu Leu Phe Val Ile Ser Leu Phe Leu Ser Asn Leu Asp
 245 250 255
 Lys Ala Leu His Ser Ala Gly Ile Asp Ser Gly Phe Ile Ile Phe Gly
 260 265 270
 Ala Asn Leu Ser Asn Pro Leu Asn Met Leu Leu Pro Leu Leu Gln Thr
 275 280 285
 Val Phe Pro Leu Asp Tyr Ile Leu Ile Thr Ile Ile Ile Met Tyr Phe
 290 295 300
 Ile Phe Thr Ser Met Ala Gly Ile Arg Asn Ile Gly Ile Trp Phe Phe
 305 310 315 320
 Trp Ile Arg Leu Tyr Lys Ile Arg Arg Gly Arg Thr Arg Pro Gln Ala
 325 330 335
 Leu Leu Phe Leu Cys Met Ile Leu Leu Leu Ile Val Leu His Thr Ser
 340 345 350

Tyr Met Ile Tyr Ser Leu Ala Pro Gln Tyr Val Met Tyr Gly Ser Gln
 355 360 365
 Asn Tyr Leu Ile Glu Thr Asn Ile Thr Ser Asp Asn His Lys Gly Asn
 370 375 380
 Ser Thr Leu Ser Val Pro Lys Arg Cys Asp Ala Asp Ala Pro Glu Asp
 385 390 395 400
 Gln Cys Thr Val Thr Arg Thr Tyr Leu Phe Leu His Lys Phe Trp Phe
 405 410 415
 Phe Ser Ala Ala Tyr Tyr Phe Gly Asn Trp Ala Phe Leu Gly Val Phe
 420 425 430
 Leu Ile Gly Leu Ile Val Ser Cys Cys Lys Gly Lys Lys Ser Val Ile
 435 440 445
 Glu Gly Val Asp Glu Asp Ser Asp Ile Ser Asp Asp Glu Pro Ser Val
 450 455 460
 Tyr Ser Ala
 465

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GTTCCGAAAT AAAAGATTTT GCAAACCACT TTCCTACGTA CGTCCACTGT AGTTTTTGCA 60
 GATACAACAC TAGCTGTAGC AAAGCCTATG TAAATCATAT GATGAGCTTT CATAGTAACC 120
 GTCCAAGCAA AAGGTTTTGT ATTTTAAAGA AGCATTGAGA AAATCTCCGG GGCATTACTC 180
 TAGTGTGCCCT TAATTGTGAT TTCCTAAGTG ATGTTTCTGG CTTAGATAAT ATGGCTACAC 240
 ACTTAAGTCA ACATAAACT CATACTTGCC AAGTTGTAAT GCAGAAAGTT TCTGTTTGTA 300
 TCCCAACTTC TGAGCACCTT TCTGAATTAA AAAAAGAAGC TCCCGCAAAG GAACAAGAAC 360
 CTGTGTCTAA GGAAATTGCA AGACCTAACA TGGCTGAAAG AGAAACAGAA ACATCAAATT 420
 CTGAAAGTAA ACAAGATAAA GCTGCTTCTT CAAAAGAAAA AAATGGATGT AATGCAAATT 480
 CATTTGAAGG CTCATCAACA ACAAAAAGTG AAGAAAGCAT AACAGTTTCA GATAAGGAAA 540
 ATGAAACCTG TCTTGCAGAC CAGGAACTG GCTCAAAAAA CATCGTCAGT TGTGATTCAA 600
 ATATTGGTGC AGATAAAGTG GAAAAGAAAA AACAAATACA ACACGTTTGT CAGGAAATGG 660
 AGTTGAAGAT GTGCCAAAGT TCAGAAAACA TAATCTTATC TGATCAGATT AAAGATCACA 720
 ACTCCAGTGA AGCCAGATTT TCTTCAAAGA ATATTAAGGA TTTGCGATTA GCATCAGATA 780
 ATGTAAGCAT TGATCAGTTT TTGAGAAAAA GACATGAACC TGAATCTGTT AGTTCTGATG 840
 TTAGCGAGCA AGGCAGTATT CATTTGGAAC CTCTGACTCC ATCCGAGGTA CTTGAGTATG 900
 AAGCCACAGA GATTCCTCAG AAAGGTAGTG GTGATCCTTC AGCCAAGACT GATGAAGTAG 960
 TGTCTGATCA AACAGATGAC ATTCCTGGAG GAAATAACCC TAGCACAACA GAGGCAACAG 1020
 TAGACCTGGA AGATGAAAAA GAAAGAAGTT GAAATTAGTC ATTTTAAGTT TCAGTGATACC 1080

AACGATAAGG GCATTTGGAA CAGTGCTATC AGGTGAGCTC AGTGGTGCTG TTGTAGGTTC 1140
AGAAATGGAA ATATGTAAGG GAGGTCACAC ATACACTTTA CCTGTATGTT CAACCTATGT 1200
TATCAAACAA ATCAATTCAC CAATAATAGC ATGATTAGTA GGGATTCCCA AAAAGTTTTT 1260
AAAAACACGA ACAGGATTTT AATGATAATT AAATTTGCAG TGGAAAGGTC TCATTTAATG 1320
GTTTTCAAGG AAATGGGATT TGGTTGCTGA CATGAATTGA TGATATTAGT AATATTTATA 1380
AAGCCTTTCA AACTTCCATC AATCCTAAGC TAAAAATCTT TATTACCTGT ATATCCTTTT 1440
CAGTTAACTG AGAGGAAGGG ATTTGGAAAC CATGTACTTT TGGGGAGTAA TTGATTAAAA 1500
ACAATGGCTG ATTGGCATTG TTAATGAAGG CTTTATTTGT GAGGATGATG CTGGTAAATG 1560
GAGCATGCTT AGAGTACTAA ATTGATCTAA TGAGAATTTG GATGAACATA AACTTAATTT 1620
TGGATTTAAT ATAACATTCC AGTCAGACGC ATGTAAACAG AATATTTGAA TCTTTGTACC 1680
TCCATACAAG TGTTAGCCTG CCAGGCTGTA AGCTTACCTT AATTAACTT TCAGTGAAAG 1740
TGGAATTATT AAGATATAAA TTTATATTTG TGCTTTTTGT CAGTGTGTAA GCTGTGTAGA 1800
AATTCCTTGA TGTATTAGTT GTATTAATGT AAAGTAGAAA CCCATTGTTG AAACCTCCTGT 1860
AGCTATTATG CTTTAAATAT TGTTTTAATG ATCTTCCTTA GAAATAGGCC CATAAAAATG 1920
GTCTGGAAGC CAAACCAAAG TATGGTATAA TGTAGATATT GTAAAGCAGT AAACGTAAAA 1980
CATGTCCTGG CATGTATTCA GCCATGTTTA AGTGACTTTT CTGTAATTGT AAAATAAAAA 2040
CTTCAAATGG GACCTAAAAC AGTGATGTAA AAGAACTGGT TTTGGAAATT TAGCCTAATT 2100
TATCTATAAG ATGGCTGCTA AATTGATTTT TCAGTTCTTT TTATCATCTA GAATATAATA 2160
GATATAGAAA TGAATAATAT GAAGAACAGT AGTTTGCTTT GAAATACTAA TAACTTTTAA 2220
TTTAAAATGC TTCATTTTAA CTTCTTAAAA TGTGCTTTGG ATTCTTAAAT TTTGTTTCAC 2280
TGAATGTTCA ATGTTTTTAA TGGCGATTAA AATACTCTGC TGTATATAGT AGTTTTTGTAG 2340
TAAATATTTG CAATAAAAAAT CTGCCCCCGA ATAAAAAAA AAAAAAAAAA AAAAAAAAAA 2400
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2460
AAAAAAAAA AAAAAAAAAA AAAAAA 2487

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Met Ser Phe His Ser Asn Arg Pro Ser Lys Arg Phe Cys Ile Phe
1 5 10 15
Lys Lys His Ser Glu Asn Leu Arg Gly Ile Thr Leu Val Cys Leu Asn
20 25 30
Cys Asp Phe Leu Ser Asp Val Ser Gly Leu Asp Asn Met Ala Thr His
35 40 45
Leu Ser Gln His Lys Thr His Thr Cys Gln Val Val Met Gln Lys Val
50 55 60
Ser Val Cys Ile Pro Thr Ser Glu His Leu Ser Glu Leu Lys Lys Glu
65 70 75 80
Ala Pro Ala Lys Glu Gln Glu Pro Val Ser Lys Glu Ile Ala Arg Pro
85 90 95

Asn	Met	Ala	Glu	Arg	Glu	Thr	Glu	Thr	Ser	Asn	Ser	Glu	Ser	Lys	Gln	100	105	110	
Asp	Lys	Ala	Ala	Ser	Ser	Lys	Glu	Lys	Asn	Gly	Cys	Asn	Ala	Asn	Ser	115	120	125	
Phe	Glu	Gly	Ser	Ser	Thr	Thr	Lys	Ser	Glu	Glu	Ser	Ile	Thr	Val	Ser	130	135	140	
Asp	Lys	Glu	Asn	Glu	Thr	Cys	Leu	Ala	Asp	Gln	Glu	Thr	Gly	Ser	Lys	145	150	155	160
Asn	Ile	Val	Ser	Cys	Asp	Ser	Asn	Ile	Gly	Ala	Asp	Lys	Val	Glu	Lys	165	170	175	
Lys	Lys	Gln	Ile	Gln	His	Val	Cys	Gln	Glu	Met	Glu	Leu	Lys	Met	Cys	180	185	190	
Gln	Ser	Ser	Glu	Asn	Ile	Ile	Leu	Ser	Asp	Gln	Ile	Lys	Asp	His	Asn	195	200	205	
Ser	Ser	Glu	Ala	Arg	Phe	Ser	Ser	Lys	Asn	Ile	Lys	Asp	Leu	Arg	Leu	210	215	220	
Ala	Ser	Asp	Asn	Val	Ser	Ile	Asp	Gln	Phe	Leu	Arg	Lys	Arg	His	Glu	225	230	235	240
Pro	Glu	Ser	Val	Ser	Ser	Asp	Val	Ser	Glu	Gln	Gly	Ser	Ile	His	Leu	245	250	255	
Glu	Pro	Leu	Thr	Pro	Ser	Glu	Val	Leu	Glu	Tyr	Glu	Ala	Thr	Glu	Ile	260	265	270	
Leu	Gln	Lys	Gly	Ser	Gly	Asp	Pro	Ser	Ala	Lys	Thr	Asp	Glu	Val	Val	275	280	285	
Ser	Asp	Gln	Thr	Asp	Asp	Ile	Pro	Gly	Gly	Asn	Asn	Pro	Ser	Thr	Thr	290	295	300	
Glu	Ala	Thr	Val	Asp	Leu	Glu	Asp	Glu	Lys	Glu	Arg	Ser				305	310	315	

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

TTTATTTTTC AAATCATAAT TTTAAAAATGA TAGATACCAT TTTGTGATAA CAACAATTCA 60
GAAAAACAATT TTCTATCCTC TTAGTTGAAA GAATGTAGGT ACAGTTTGGA TACTTGTACT 120
TTAATTTTATAG AGTAAACATC TGCATTATAC TCTTATAGAT AATAGAATTA TTTAGTTAAG 180
AAATTCCTTTA CAGTAAATGA GATAATGTGT GAAAAAGTAT TTTGTAAATG CTGAGGATTC 240
TACAAATGAT AGTTGTTATT TTCATGTGTA TTTGTAAGAT CATGTCCATT TCATGAATAT 300
AGGACTTCAC ATAAAAAAG ACTTTCTCAA GACAACTTTA TATTCTAGTA TTTTCTGT 360
GTAAAAAGTA TTAACATATT ACTTTTATTT TGTATACAT TTATTTTAAAT ATCCATGTGT 420
TTATTATAGT AAATTTGAAA TGAAATCCTG AAAAAACAGAA TTTTTTTAAA CACAGACCTC 480
ACACCAATAT TAATTTTTTTC TCTACATAAT TTAAAACTAC ATAAATTAAG TACTTAAAAT 540
TTATATTGAA GGCCACCAAG AACTTAGGTT GAATCTTAGA AAATTTAAAT AACTATTTTT 600
AAAGTTACCC AACTTAATAT TTTAATTTTT TAATATTTAT CTTCTTTAC TAATTCTTGA 660
TAAATAATAG CATTAGACTT GATAAAATAA AAAAGAATTT TAGAGTAGAA TTAATATATC 720
AAAAGGGGTA TATCAACCAA ATTGGTGTCA GATTGTATTC ATTCTCTCAT CACATAAAGA 780
TTTTTCTTTT GATAGGTGAT GCTCATATGA ACCTTTGGTT TAGAATCTAT ATATGTACAT 840
GTGTATGTAT GTAGATAGTA TGGTTGTATA CACACATATA TACCAAACAC CATGAATTTT 900
AGCAGTCTGT GATGATCAGC AAAAAAGCAC ATAAAGTAAA ATTAGTTGAC CATGCTAAAT 960
TCAATTCTGG AATTTTTTTTT TATTTGGGCA TTTCTAGAAC TTTTACATT TGAAAGTACA 1020
TGATGAGTAT TAGTAACGAT GACTTATGTA TAATCAGAAT CTTTATGACA ATTTAGTTTT 1080
ACAAGGTCAG AAGAGATGAG TTTGCTAAAC CCAGCTGTGA TACCTCAGTT GGAAAGGGAA 1140
TTCAAAGGTA TGCTTTGTAG AACAGAAAAG TATAGTTTTT TTTTCATGAA CTTTAATCAT 1200
TTTCTGTTTT TCCTCTATGT GAGTCAGCTA CAAAAGTGGT CTAATTTTTTA CAACAGTAGA 1260
ACTTCCTCCT TTTCTACTGT AATCTTCCCA CTGACTTTAC TGCACAGGTA TGAAATACTA 1320
GTGTATTGGA TCTTCAGTAA CCTTTTTATT TCCTAGATGA TTGAAATATA GGTATTTACT 1380
CCATTTAAAC CAGGTGATAA GATGATGTAA ATACTCAGGG AGGGTATTAA CTTGTTACTT 1440
TTGCTCGTTT GGGGTGTAAA GGCCATGAC TGAATAATCT TCAATTCATG ATTCTAGAGT 1500
AAGTTTAAAT TGGAAAAAGG GGCTTCACAC ATGGTGGTGG TTGAACATTG ATTCTTTTAT 1560
ACTTTAAAG ATGAAAATGT TTTGTGGACT GATACATTTT ATCTTACTGA ATATGAATTG 1620
TTTATGTATC TCTACTGTCA AATAGCCTTT TTGAACTCA GGAAAGACAA AGGTTCAATT 1680
ACACCACTTT TGTCAATAAG CAAACCAGGT ATTTTTTTTT TCTCCTGTTG TCTGGATATG 1740
GCAATAGATT TTTTAAATTG CTGTGAGAAC CCATATATGA AAAGAGAGGA GTTGAATTGT 1800
GTGTGCCTTT TATGTCTTGA GATTTATATG TGGAAAAGAC GACATCTACT TCAAACGTGA 1860
TTTTTTTCGT TTTTTTTTTT TTTTTGGGGA AGGGGGGAGA ACGGGGTCTT GCTCTGTCGC 1920
CCAGGCTGGA GTGCAGTGGC GCGATCTCAG CTGACTGCAA CCTCCACCTC CCGGGTTCAA 1980
GGGATTCTGC CTCAGCCTCC CGAGTAGCTG AGACCACAGG TGCGTGCCAC CACACCCGGC 2040
TAATTTTTTT GTATTTTTAG TAGAGACGGG GTTTAGTAGA GACGGATCAC TCCTGACCAC 2100
GTGATCCGCC CACCTCGGCC TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCACCCCC 2160
GGCCTGTATT TTCAGAGAGG AGAGCTTGGT GTTTTTGTGG TGCCAAGTGG TAAGATAATG 2220
TCTCTTTGAG GCTTCCTATG GACTGCCTTT ATTTTAGTAA ACTCAAGACA CCAGTTAACC 2280
TCAACAGAGT TTTGGCCTTA TTAGAATTTG TTGTGCATCT TATTGAAAGC CAGGTTTACA 2340
TCACCTCACC CCATTATTCT TTTTAGTTAA ATAAATTTAC CATGCCAAGT AACAGAATG 2400
GAGCAAATTG GTTGATCTTT AAGGCAGTAG GTTTGACTAG CTAGCTATCA TTATTGTCAC 2460
ATCTAATGCT AGGCACCAGA AACCATTTGA GCCAGGAGTG TGAATGAATA ATTCCAGAG 2520
ACACTTTAGA CATTTTTTAA TGTTTTATAT GACATTTTAC ATTTGTGTGA TTGCCTTAGA 2580
TATTAAATTT TCCTAGTGCT GATAAAAAACA GCAACATTCA TAACTTATTT TATATATTGT 2640
TCCAAAGAAA AGAATTTGTT TTAATGGTTT CAAAATAACT GCACCTGAAT TTGTTTATGT 2700
GCCTTAAAGT CTCTAGTGCT ATTTCAACTT TTTTTTCAAT CTAAATGAAG CTTACCTTAG 2760
ATAAGGTTCA TATTTGTTTC CTATAGAGTA AATAAACTTC CCCTTCTTAA ATTGTGTAAT 2820
AAGCACCAAC GTGTGGTTGC TTGGCAGAAT GAGAATGTTA AGGGAGATTG TTGGATGTTT 2880
GGAGTTTCAT TATATTTTTT GTTTTTATTT TTTGATACCT AGGTGCTTTT TAAATATATC 2940
AGACAAATAT CTATCTTACA TTGATTAAAC CCGTGTAAT TCATTTGCAG TATCTACATC 3000
GAATGTCAAA AAAGTATACT TATTTTTGTT CCATACTTAT GTACAATTTT TTCCCTCTTC 3060
AGGCTTTTTT ATTTACCTTT TTGAAAAGC ACTTACTCTC CCCTTCCCTA TCACCCCTCC 3120
CCCAAGGTTT CTTTATTTAA ATTTTATTG AGAGTTGTTG GAGCTCTAAG ACAATACAAA 3180
TTTAGAGTTG AACAAAAGTA TAATCTGCTT TACAACTAGT ATAGACCTAA GGTCATTTGC 3240
TTTCAATTAG AGGCTCCAGA GTCTTCATAG TGGAAAGAAT GCTTTGTATT TAATTGTTCT 3300
TAGTTAAGTT GTAGCACGTG AATACTTACT TACATGTTTT GTTTAAATAT ACTTCTTGCA 3360

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TAGTTTAATT TTTTAAAAGT TGTATCTAAT AAAATGTCTT TTAACCATTA TTAAGTGGT 3420
 ATATGGTTGT ATTAATTTT GTTTACGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3480
 AAAAAAAAAA AAAAA 3495

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ser Lys Lys Tyr Thr Tyr Phe Cys Ser Ile Leu Met Tyr Asn Phe
 1 5 10 15
 Phe Pro Leu Gln Ala Phe Ser Phe Thr Phe Leu Lys Lys His Leu Leu
 20 25 30
 Ser Pro Ser Leu Ser Pro Leu Pro Gln Gly Phe Phe Ile
 35 40 45

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GTTGATCCAT CTGAGAAAAGG GATCATGAAC TAGACAGAAT GAACAGCCTT AGAGGCACAG 60
 ACTCTTGAAC GGGACGGTGG TGGTATGACT AGTGCAGAGT GTTTAGAGAT CACTCAGTTT 120
 TTAAAGACTG GCCTTTATCG TGTCTCAGTG CAGCCGAGGC AGAGCCTTTG AAGGATGCGA 180
 TGTTGTCATT CTTACTAATC TAGTCCAGCC GCTGAGGTGA CTTTCAACGG CAGACCGTCT 240
 CCTGAGCGCC CCAGGTAGAA TTTCAAAAGT CTCCGGGACC ATTATGGCAG TCAAGTGGAC 300
 GGGTGGGCAT TCTTCTCCTG TCCTCTGCCT GAATGCAAGT AAAGAAGGGC TGCTGGCTTC 360
 TGGAGCAGAG GGCAGGATC TCACGGCTTG GGGTGAAGAT GGAACCTCCAT TAGGACACAC 420
 GCGGTTCCAA GGGGCTGATG ATGTTACCAG TGTCTTATTT TCTCCCTCCT GTCCACCAA 480
 GCTCTATGCC TCACATGGAG AAACCATTAG TGTACTGGAT GTCAGGTCCC TCAAAGATTG 540
 CTTGGACCAT TTTCATGTGA ATGAAGAAGA AATCAATTGT CTTTCATTGA ATCAAACGGA 600
 AAACCTGCTG GCTTCTGCTG ACGACTCTGG GGCAATCAAA ATCCTAGACT TGGAAAACAA 660
 GAAAGTTATC AGATCCTTGA AGAGACATTG CAATATCTGC TCCTCAGTGG CTTTTCGGCC 720
 TCAGAGGCCT CAGAGCCTGG TGTATGTGG AATTGGATATG CAGGTGATGC TGTGGAGTCT 780
 TCAAAAAGCC CGACCACTCT GGATTACAAA TTTACAGGAG GATGAAACAG AAGAAATGGA 840
 AGGCCACAG TCACCTGGTC AGCTCTTAAA CCCTGCCCTA GCCCATTCTA TCTCTGTGGC 900


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TTCGTGTGGT AATATTTTTA GTTGTGGTGC AGAAGATGGT AAGGTTTCGAA TCTTTCGGGT 960
GATGGGAGTT AAGTGTGAAC AGGAAGTGGG ATTTAAGGGC CACACTTCAG GGGTATCCCA 1020
GGTCTGCTTT CTCCAGAAAT CCTATTTGCT GCTTACTGGA GGAATGATG GGAAGATCAC 1080
GTTGTGGGAT GCAAACAGTG AAGTTGAGAA AAAACAGAAG AGTCCCACAA AACGTACCCA 1140
CAGGAAGAAA CCTAAAAGAG GAACTTGCAC CAAGCAGGGT GGAAATACTA ACGCTTCAGT 1200
AACAGATGAG GAAGAACATG GCAACATTTT ACCGAAGCTA AATATTGAAC ATGGAGAAAA 1260
AGTGAAGTGG CTCTTGGGTA CAAAAATAAA GGGACACCAA AATATATTAG TAGCTGATCA 1320
AACTAGTTGT ATATCTGTAT ACCCCTTAAA TGAATTTTAA ATCCAATAAA AACATTTGAA 1380
GAAAAAAAAA AAAAAAAAAA                                     1398

```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

Met Ala Val Lys Trp Thr Gly Gly His Ser Ser Pro Val Leu Cys Leu
 1             5             10             15

Asn Ala Ser Lys Glu Gly Leu Leu Ala Ser Gly Ala Glu Gly Gly Asp
      20             25             30

Leu Thr Ala Trp Gly Glu Asp Gly Thr Pro Leu Gly His Thr Arg Phe
      35             40             45

Gln Gly Ala Asp Asp Val Thr Ser Val Leu Phe Ser Pro Ser Cys Pro
      50             55             60

Thr Lys Leu Tyr Ala Ser His Gly Glu Thr Ile Ser Val Leu Asp Val
      65             70             75             80

Arg Ser Leu Lys Asp Ser Leu Asp His Phe His Val Asn Glu Glu Glu
      85             90             95

Ile Asn Cys Leu Ser Leu Asn Gln Thr Glu Asn Leu Leu Ala Ser Ala
      100            105            110

Asp Asp Ser Gly Ala Ile Lys Ile Leu Asp Leu Glu Asn Lys Lys Val
      115            120            125

Ile Arg Ser Leu Lys Arg His Ser Asn Ile Cys Ser Ser Val Ala Phe
      130            135            140

Arg Pro Gln Arg Pro Gln Ser Leu Val Ser Cys Gly Leu Asp Met Gln
      145            150            155            160

Val Met Leu Trp Ser Leu Gln Lys Ala Arg Pro Leu Trp Ile Thr Asn
      165            170            175

Leu Gln Glu Asp Glu Thr Glu Glu Met Glu Gly Pro Gln Ser Pro Gly

```

CCGGAGGTAG CTACCACGGC CTGTGTCAAC GACTAAAGCT CAGTACAGC GGCGCCCTCA 60

180 185 190
Gln Leu Leu Asn Pro Ala Leu Ala His Ser Ile Ser Val Ala Ser Cys
195 200 205
Gly Asn Ile Phe Ser Cys Gly Ala Glu Asp Gly Lys Val Arg Ile Phe
210 215 220
Arg Val Met Gly Val Lys Cys Glu Gln Glu Leu Gly Phe Lys Gly His
225 230 235 240
Thr Ser Gly Val Ser Gln Val Cys Phe Leu Pro Glu Ser Tyr Leu Leu
245 250 255
Leu Thr Gly Gly Asn Asp Gly Lys Ile Thr Leu Trp Asp Ala Asn Ser
260 265 270
Glu Val Glu Lys Lys Gln Lys Ser Pro Thr Lys Arg Thr His Arg Lys
275 280 285
Lys Pro Lys Arg Gly Thr Cys Thr Lys Gln Gly Gly Asn Thr Asn Ala
290 295 300
Ser Val Thr Asp Glu Glu Glu His Gly Asn Ile Leu Pro Lys Leu Asn
305 310 315 320
Ile Glu His Gly Glu Lys Val Asn Trp Leu Leu Gly Thr Lys Ile Lys
325 330 335
Gly His Gln Asn Ile Leu Val Ala Asp Gln Thr Ser Cys Ile Ser Val
340 345 350
Tyr Pro Leu Asn Glu Phe
355

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CCGGAGGTAG CTACCACGGC CTGTGTCAAC GACTAAAGCT CAGTACAGC GGCGCCCTCA 60
GACAGCTGGG AGGGTGGCTC TGGCCGGGAG CGGCGGCCCG TGAGCTACCG CGAGGAGGAG 120
CGGCGGAGGC GACCTCGGCC CGGCCCTGCA CTGGCCGCCC GGCAGGCGCG ACATGAGCCT 180
GGTCTGGCAT CCGCGGGATG CTCCTTAAGC CCCTTCTCCG GCTGTAAACC TCCGGGGAAC 240
GGTTGTGACC ACACCGACAC GTATTTTACA GATAAATCAT TCTTGCGGCG GCGGGTTCGAA 300
CACGTTTATT TATTTTAT TTTCTCAACA AGCTTTTACC CAGCACCTGT CCAGTGAAAC 360
AACTTGATAA TCGTTTCGAG GGGCGTCCGC CGGGTTAGGA AGCCTGCGC TGGCAGCTTG 420
TGGAAGCCTC ATTTGCAAAG CCACCCCTCA GATGTTTTGA AGATCGTGAC GTCTTGTAAC 480

TAGCAGTGTG TGCACAGAAT CCTACTCAAG GAACGTCTTG GCCCAGCGAT GCAAAGAAGT 540
 GAAGTTTCAA GCTGGAAGAG CCTGTATTGT CCTCACAATA GTATAGAAGA ATTCAAGAGA 600
 GGAGAGAGAG ACAGCACCGA ATGAAGACTG TAAAAGAAAA GAAGGAATGC CAGAGATTGA 660
 GAAAACTGTC CAAGACTAGG AGGGTAACCC AGAGGAAACC GTCTTCAGGG CCTGTTTGCT 720
 GGTATGCCCT TCGAGAACCT GGGGATCCCG AAAAATTAGG GGAATTTCTT CAGAAAGACA 780
 ATATCAGCGT GCATTATTTT TGTCTTATCT TATCTAGTAA GCTGCCTCAG AGGGGCCAGT 840
 CCAACAGAGG TTTCCATGGA TTTCTGCCTG AAGACATCAA AAAGGAGGCA GCGGGGCTT 900
 CTAGGAAGAT CTGCTTTGTG TGCAAGAAAA AGGGAGCTGC TATCAACTGC CAGAAGGATC 960
 AGTGCCTCAG AAACCTCCAT CTGCCTTGTG GCCAAGAAAG GGGTTGCCTT TCACAATTTT 1020
 TTGGAGAGTA CAAATCATTT TGTGACAAAC ATCGCCCAAC ACAGAACATC CAACATGGGC 1080
 ATGTGGGGGA GGAAAGCTGC ATCTTATGTT GTGAAGACTT ATCCCAACAG AGTGTTGAGA 1140
 ACATCCAGAG CCCGTGTTGT AGTCAAGCCA TCTACCACCG CAAGTGCATA CAGAAATATG 1200
 CCCACACATC AGCAAAGCAT TTCTTCAAAT GTCCACAGTG TAACAATCGA AAAGAGTTTC 1260
 CTCAAGAAAT GCTGAGAATG GGAATTCATA TTCCAGACAG AGATGCTGCC TGGGAACTCG 1320
 AGCCAGGGGC TTTCTCAGAC TTATATCAGC GCTATCAGCA CTGTGATGCC CCCATCTGTC 1380
 CGTATGAACA AGGCAGAGAC AGCTTTGAGG ATGAAGGGAG GTGGTGCCTC ATTCTGTGTG 1440
 CTACATGCGG ATCCCACGGA ACCCACAGGG ACTGCTCCTC TCTTAGATTT AACAGTAAGA 1500
 AATGGGAGTG TGAGGAGTGT TCACCTGCTG CAGCCACAGA CTACATACCT GAAAACTCAG 1560
 GGGACATCCC TTGCTGCAGC AGCACCTTCC ACCCTGAGGA ACATTTCTGC AGAGACAACA 1620
 CCTTGGAAGA GAATCCGGGC CTTTCTTGGA CTGATTGGCC AGAACCTTCC TTATTAGAAA 1680
 AGCCAGAGTC CTCTCGTGCG AGGAGGAGCT ACTCCTGGAG GTCCAAGGGT GTCAGAATCA 1740
 CTAACAGCTG CAAAAAATCC AAGTAACACC TTCTGAGTAG CTGCTGTCCC ACACAATAGG 1800
 GTATGAAGCT GCGCTCCTCC ATCGGGTTTG GGGAGGGAGC ACTCTGGGAC TGTGAGACAA 1860
 GGAAGCAGGG CCAGCAGTGA GACTATGAGC CAAGCAAAGA GAAGTCTCAG TGGAGCATGA 1920
 GGAGGGAGCA GTCCAGATGC CAACAAGGAA ATGCGTTTAT GGCTACAAGA GTGCCTCTGC 1980
 TTTCTCCTCC TCTCCTCCCA CCAAGGATTC TTCCACCTTA ATCTTGTTTT CATATGCCTC 2040
 TTCTTACTTC ACCCATGTTT GTTGTTATGC AAATAAAGGT TTTCTCTCCC AAAAAAAAAA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 2132

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met Lys Thr Val Lys Glu Lys Lys Glu Cys Gln Arg Leu Arg Lys Ser
 1 5 10 15
 Ala Lys Thr Arg Arg Val Thr Gln Arg Lys Pro Ser Ser Gly Pro Val
 20 25 30
 Cys Trp Leu Cys Leu Arg Glu Pro Gly Asp Pro Glu Lys Leu Gly Glu
 35 40 45
 Phe Leu Gln Lys Asp Asn Ile Ser Val His Tyr Phe Cys Leu Ile Leu
 50 55 60
 Ser Ser Lys Leu Pro Gln Arg Gly Gln Ser Asn Arg Gly Phe His Gly
 65 70 75 80
 Phe Leu Pro Glu Asp Ile Lys Lys Glu Ala Ala Arg Ala Ser Arg Lys

95

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```
GTCACGTGGA ACCTCTTAAT CTCAGCATCC GGAGCTCCAG GAAGGGAAAA TTTCAAGTCA 60
GATAGAATTC TATATATACC ATTTCTTTTG AACCTTCAGC CCTCAAGATT CCAACATCAT 120
GACCTCAGTT TCAACACAGT TGTCCCTTAGT CCTCATGTCA CTGCTTTTGG TGCTGCCTGT 180
TGTGGAAGCA GTAGAAGCCG GTGATGCAAT CGCCCTTTTG TTAGGTGTGG TTCTCAGCAT 240
TACAGGCATT TGTGCCTGCT TGGGGGTATA TGCACGAAAA AGAAATGGAC AGATGTGACT 300
TTGAAAGGCC TACTGAGTCA AACCTCACCC TGAAAACCTT TGCGCTTTAG AGGCTAAACC 360
TGAGATTTGG TGTGTGAAAG GTTCCAAGAA TCAGTAAATA AGGGAGTTTC ACATTTTTC 420
TTGTTTCCAT GAAATGGCAA CAAACATACA TTTATAAAAT GAAAAAAAAA TGTTTTCTTT 480
ACAACAAATA ATGCACAGAA AAATGCAGCC TATAAATTGC TAGTTAGGTA GTCAAAGAAG 540
TAAGATGGCT GAAATTTACA TAAGTAATAT TTCATAATCT TAGAATTCTC TCAAAGCATG 600
TGAAATAGGA AGAAGGAAGT TCTTGCCCAG AATCTTAGGA AATCACCCT GTTCGGTTAT 660
AATCACTGCC TCCTGAATCG TTGAGGAGTC TTTTAAATTA GATTTTGTGTT TTGTTGTCTC 720
CCAAGTTAAT ATTATATTTA GATATCAGAG AGTCAGGCAA AAAGGAAAAC TTTTATCTCT 780
AGGGAAAAAA CATTTAGAAA AATGTATTCA GTGTATCTAA TACTGAAATG CGGAAAAAAA 840
TTTAATGTTA AAAAAAACT ATAGACATTG ACATGGAAAA GAGATTTAAT GTTTTGAAAA 900
AAAAACTTTA TATTAAGTGA GTAACATCCT CCTGATGAGA AGTACTATAT TAAATATAAA 960
CCCATATATG TATAAAAAAA AAAA                                     984
```

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```
Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu
 1             5             10             15

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala
      20             25             30

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu
      35             40             45

Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met
      50             55
```

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

G TTCCTACAG CGGTGAGAGT GAAATGTG

28

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

C CGATACACC AAAGTCTCAT CCCTAAAT

28

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

G AGCTAGTGT GAAGGACAAT AAGCAGAA

28

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GTCGCTAACA TCAGAACTAA CAGATTCA

28

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAGATACTGC AAATGAATTT ACACGGGT

28

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GTCACACTTA ACTCCCATCA CCCGAAAG

28

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCTGAGGCAC TGATCCTTCT GGCAGTTG

28

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TGAGGGCTGA AGGTTCCAAA GAAATGGT

28

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGCTTTTTTT TTTTTTTTGA CAAGATGGCG GCAGGAGGCA GTGGCGTTGG TGGGAAGCGC 60
 AGCTCGAAAA GCGATGCCGA TTCTGGTTTC CTGGGGCTGC GGCCCACTTC GGTGGACCCA 120
 GCGCTGAGGC GGCGGCGGCG AGGCCCAAGA AATAAGAAAGC GGGGCTGGCG GCGGCTTGCT 180
 CAGGAGCCGC TGGGGCTGGA GGTGACCAG TTCCTGGAAG ACGTGC GGCT ACAGGAGCGC 240
 ACGAGCGGTG GCTTGTGTGC AGAGGCCCA AATGAAAAAC TCTTCTTCGT GGACACTGGC 300
 TCCAAGGAAA AAGGGCTGAC AAAGAAGAGA ACCAAAGTCC AGAAGAAGTC ACTGCTTCTC 360
 AAGAAACCCC TTCGGGTTGA CCTCATCTC GAGAACACAT CCAAAGTCCC TGCCCCCAAA 420
 GACGTCCTCG CCCACCAGGT CCCCAACGCC AAGAAGCTCA GGCGGAAGGA GCAGCTATGG 480
 GAGAAGCTGG CCAAGCAGGG CGAGCTGCCC CGGGAGGTGC GCAGGGCCCA GGCCCGGCTC 540
 CTCACCCCTT CTGCAACAAG GGCCAAGCCC GGGCCCCAGG ACACCGTAGA GCGGCCCTTC 600
 TACGACCTCT GGGCCTCAGA CAACCCCTG GACAGGCCGT TGGTTGGCCA GGATGAGTTT 660
 TTCCTGGAGC AGACCAAGAA GAAAGGAGTG AAGCGGCCAG CACGCCTGCA CACCAAGCCG 720
 TCCCAGGCGC CCGCCGTGGA GGTGGCGCCT GCCGGAGCTT CCTACAATCC ATCCTTTGAA 780
 GACCACCAGA CCTGCTCTC AGCGGCCAC GAGGTGGAGT TGCAGCGGCA GAAGGAGGCG 840
 GAGAAGCTGG AGCGGCAGCT GGCCCTGCCC GCCATGGAGC AGGCCGCCAC CCAGGAGTCC 900
 ACATTCCAGG AGCTGTGCGA GGGGCTGCTG GAGGAGTCGG ATGGTGAGGG GGAGCCAGGC 960
 CAGGGCGAGG GGCCGGAGGC TGGGGATGCC GAGGTCTGTC CCACGCCCCG CCGCCTGGCC 1020
 ACCACAGAGA AGAAGACGGA GCAGCAGCGG CGGCGGGAGA AGGCTGTGCA CAGGCTGCGG 1080
 GTACAGCAGG CCGCGTTGCG GGCCGCCCGG CTCCGGCACC AGGAGCTGTT CCGGCTGCGC 1140
 GGGATCAAGG CCCAGGTGGC CCTGAGGCTG GCGGAGCTGG CGCGGCGGCG GAGGCGGCGG 1200
 CAGGCGCGGC GGGAGGCTGA GGCTGACAAG CCCCAGAGGC TGGGACGGCT CAAGTACCAG 1260
 GCACCTGACA TCGACGTGCA GCTGAGCTCG GAGCTGACAG ACTCGCTCAG GACCCTGAAG 1320
 CCCGAGGGCA ACATCCTTCG AGACCGGTTT AAGAGCTTCC AGAGGAGGAA TATGATCGAG 1380
 CCTCGAGAGA GAGCCAAGTT CAAACGCAAG TACAAGGTGA AGCTGGTGGA GAAGCGGGCG 1440
 TTCCGTGAGA TCCAGTTGTA GCTGCCATCA GATGCCGGAG ACTCGCCCTT CAATAAAAAA 1500
 TCTCTTCTAG CTGAAAAAAA AAAAAAAA 1528

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```
Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser
 1              5              10              15

Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro
      20              25              30

Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp
      35              40              45

Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu
      50              55              60

Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu
      65              70              75              80

Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys
      85              90              95

Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu
      100             105             110

Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val
      115             120             125

Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys
      130             135             140

Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu
      145             150             155             160

Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser
      165             170             175

Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe
      180             185             190

Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly
      195             200             205

Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg
      210             215             220

Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val
      225             230             235             240
```

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ACAAGATGGC GGC GCCGAAG GGGAGCCTCT GGGTGAGGAC CCAACTGGGG CTCCCGCCGC 60
TGCTGCTGCT GACCATGGCC TTGGCCGGAG GTTCGGGGAC CGCTTCGGCT GAAGCATTTG 120
ACTCGGTCTT GGGTGATACG GCGTCTTGCC ACCGGGCCTG TCAGTTGACC TACCCCTTGC 180
ACACCTACCC TAAGGAAGAG GAGTTGTACG CATGTCAGAG AGGTTGCAGG CTGTTTTCAA 240
TTTGTCAATT TGTGGATGAT GGAATTGACT TAAATCGAAC TAAATTGGAA TGTGAATCTG 300
CATGTACAGA AGCATATTCC CAATCTGATG AGCAATATGC TTGCCATCTT GGTGGCCAGA 360
ATCAGCTGCC ATTCGCTGAA CTGAGACAAG AACAACTTAT GTCCCTGATG CCAAAAATGC 420
ACCTACTCTT TCCTCTAACT CTGGTGAGGT CATTCTGGAG TGACATGATG GACTCCGCAC 480
AGAGCTTCAT AACCTCTTCA TGGACTTTTT ATCTTCAAGC CGATGACGGA AAAATAGTTA 540
TATTCCAGTC TAAGCCAGAA ATCCAGTACG CACCACATTT GGAGCAGGAG CCTACAAATT 600
TGAGAGAATC ATCTCTAAGC AAAATGTCCT CAGATCTGCA AATGAGAAAT TCACAAGCGC 660
ACAGGAATTT TCTTGAAGAT GGAGAAAGTG ATGGCTTTTT AAGATGCCTC TCTCTTAACT 720
CTGGGTGGAT TTTAACTACA ACTCTTGTC TCTCGGTGAT GGTATTGCTT TGGATTTGTT 780
GTGCAACTGT TGCTACAGCT GTGGAGCAGT ATGTTCCCTC TGAGAAGCTG AGTATCTATG 840
GTGACTTGGA GTTTATGAAT GAACAAAAGC TAAACAGATA TCCAGCTTCT TCTCTTGTGG 900
TTGTTAGATC TAAAACTGAA GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTGAATC 960
TTGCTCATTC TGAAATTTAA GCATTTTTCT TTTAAAAGAC AAGTGTAAAT GACATCTAAA 1020
ATTCCACTCC TCATAGAGCT TTTAAAATGG TTTCAATTGGA TATAGGCCTT AAGAAATCAC 1080
TATAAAATGC AAATAAAGTT ACTCAAATCT GTGAAGACTG TATTTGCTAT AACTTTATTG 1140
GTATTGTTTT TGTAAGTAATT TAAGAGGTGG ATGTTTGGGA TTGTATTATT ATTTTACTAA 1200
TATCTGTAGC TATTTTGTGT TTTGCTTTGG TTATTGTTTT TTTCCCTTTT CTTAGCTATG 1260
AGCTGATCAT TGCTCCTTCT CACCTCCTGC CATGATACTG TCAGTTACCT TAGTTAACAA 1320
GCTGAATATT TAGTAGAAAT GATGCTTCTG CTCAGGAATG GCCCACAAAT CTGTAATTTG 1380
AAATTTAGCA GGAAATGACC TTTAATGACA CTACATTTTC AGGAACTGAA ATCATTAATA 1440
TTTTATTGTA ATAATTAATA AAAAAAAAAA AA 1472

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
1 5 10 15
Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
20 25 30
Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
35 40 45
His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
50 55 60
Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
65 70 75 80
Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
85 90 95

Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser	Gln	Ser	Asp	Glu	Gln	Tyr	Ala			
			100					105					110					
Cys	His	Leu	Gly	Cys	Gln	Asn	Gln	Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln			
		115				120						125						
Glu	Gln	Leu	Met	Ser	Leu	Met	Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu			
	130					135					140							
Thr	Leu	Val	Arg	Ser	Phe	Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser			
145					150					155					160			
Phe	Ile	Thr	Ser	Ser	Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys			
			165					170						175				
Ile	Val	Ile	Phe	Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu			
		180						185					190					
Glu	Gln	Glu	Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser			
		195					200					205						
Ser	Asp	Leu	Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu			
	210					215					220							
Asp	Gly	Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly			
225					230					235				240				
Trp	Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp			
			245						250					255				
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	Ser			
		260						265					270					
Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	Gln	Lys			
	275					280						285						
Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	Ser	Lys	Thr			
	290					295					300							
Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	Val	Asn	Leu	Ala			
305				310						315				320				
His	Ser	Glu	Ile															

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GTGATTGGTA	CAGTAGGTTT	ATAAACAGAA	GTTTAAACTT	GTAAGCTTAA	GCTTCCGTTT	60
ATAAACAGAA	GTTTAAAATT	ATAGGTCCTG	TTTAACATTC	AGCTCTGTTA	ACTCACTCAT	120

```

CTTTTTGTGT TTTTACACTT TGTCAGATT TCTTTACATA TTCATCAATG TCTGAAGAAG      180
TTACTTATGC AGATCTTCAA TTCCAGAACT CCAGTGAGAT GGAAAAAATC CCAGAAATTG      240
GCAAATTTGG GGAAAAAGCA CCTCCAGCTC CCTCTCATGT ATGGCGTCCA GCAGCCTTGT      300
TTCTGACTCT TCTGTGCCTT CTGTTGCTCA TTGGATTGGG AGTCTTGGCA AGCATGTTTC      360
ATGTAACCTT GAAGATAGAA ATGAAAAAAA TGAACAACT ACAAACATC AGTGAAGAGC      420
TCCAGAGAAA TATTTCTCTA CAACTGATGA GTAACATGAA TATCTCCAAC AAGATCAGGA      480
ACCTCTCCAC CAACTGCAA ACAATAGCCA CCAAATTATG TCGTGAGCTA TATAGCAAAG      540
AACAAGAGCA CAAATGTAAG CTTGTCCAA GGAGATGGAT TTGGCATAAG GACAGCTGTT      600
ATTTCTAAG TGATGATGTC CAAACATGGC AGGAGAGTAA AATGGCCTGT GCTGCTCAGA      660
ATGCCAGCCT GTTGAAGATA AACAACAAAA ATGCATTGGA ATTTATAAAA TCCCAGAGTA      720
GATCATATGA CTATTGGCTG GGATTATCTC CTGAAGAAGA TTCCACTCGT GGTATGAGAG      780
TGGATAATAT AATCCACTCC TCTGCCTGGG TTATAAGAAA CGCACCTGAC TTAAATAACA      840
TGTATTGTGG ATATATAAAT AGACTATATG TTCAATATTA TCACTGCACT TATAAACAAA      900
GAATGATATG TGAGAAGATG GCCAATCCAG TGCAGCTTGG TTCTACATAT TTTAGGGAGG      960
CATGAGGCAT CAATCAAATA CATTGAAGGA GTGTAGGGGG TGGGGGTTCT AGGCTATAGG     1020
TAAATTTAAA TATTTTCTGG TTGACAATTA GTTGAGTTTG TCTGAAGACC TGGGATTTTA     1080
TCATGCAGAT GAAACATCCA GGTAGCAAGC TTCAGAGAGA ATAGACTGTG AATGTTAATG     1140
CCAGAGAGGT ATAATGAAGC ATGTCCMACY TCCCACCTTC CATCATGGCY TGAACCYKGG     1200
RGAAGAGGA AGTCCATTCA GATAGTTGTG GGGGGCCTTS GAATTTTCAT TTTCATWWAC     1260
GTTCTTCCCC TTCTGGCCAA GATTTGCCAG AGGCAACATC AAAAACCAGC AAATTKTAAT     1320
TTTGTCCTCC AGSGTTGCTA GGGTGGCATG GYTCCCCATT TSGGGTCCAT CCTAWACTTC     1380
CATGGGACTC CCTATGGCTG AAGGCCTTAT GAGTCAAAGG ACTTATAGCC AATTGATTGT     1440
TTTAGGCCAG GTAAGAATGG ATATGGACAT GCATTTATTA CYTYTTAAAA TTATTATTTT     1500
AAGTAAAGC CAATAACAA AAANGNAAAG GCAAAAAAAA AAAAAAAA AAAAAAAA     1560
AAAAAAA AAA                                     1573

```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```

Met Ser Glu Glu Val Thr Tyr Ala Asp Leu Gln Phe Gln Asn Ser Ser
1           5           10           15
Glu Met Glu Lys Ile Pro Glu Ile Gly Lys Phe Gly Glu Lys Ala Pro
20           25           30
Pro Ala Pro Ser His Val Trp Arg Pro Ala Ala Leu Phe Leu Thr Leu
35           40           45
Leu Cys Leu Leu Leu Leu Ile Gly Leu Gly Val Leu Ala Ser Met Phe
50           55           60
His Val Thr Leu Lys Ile Glu Met Lys Lys Met Asn Lys Leu Gln Asn
65           70           75           80
Ile Ser Glu Glu Leu Gln Arg Asn Ile Ser Leu Gln Leu Met Ser Asn
85           90           95
Met Asn Ile Ser Asn Lys Ile Arg Asn Leu Ser Thr Thr Leu Gln Thr
100          105          110
Ile Ala Thr Lys Leu Cys Arg Glu Leu Tyr Ser Lys Glu Gln Glu His
115          120          125
Lys Cys Lys Pro Cys Pro Arg Arg Trp Ile Trp His Lys Asp Ser Cys
130          135          140
Tyr Phe Leu Ser Asp Asp Val Gln Thr Trp Gln Glu Ser Lys Met Ala
145          150          155          160

```

Cys Ala Ala Gln Asn Ala Ser Leu Leu Lys Ile Asn Asn Lys Asn Ala
165 170 175
Leu Glu Phe Ile Lys Ser Gln Ser Arg Ser Tyr Asp Tyr Trp Leu Gly
180 185 190
Leu Ser Pro Glu Glu Asp Ser Thr Arg Gly Met Arg Val Asp Asn Ile
195 200 205
Ile His Ser Ser Ala Trp Val Ile Arg Asn Ala Pro Asp Leu Asn Asn
210 215 220
Met Tyr Cys Gly Tyr Ile Asn Arg Leu Tyr Val Gln Tyr Tyr His Cys
225 230 235 240
Thr Tyr Lys Gln Arg Met Ile Cys Glu Lys Met Ala Asn Pro Val Gln
245 250 255
Leu Gly Ser Thr Tyr Phe Arg Glu Ala
260 265

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAGTTATATG	ACACTCAAAG	GAAAAGCAAA	AGAGCATTA	GAAGTGTCTG	TTTTTGTTAT	60
TGCCATTTCA	TAAATATTTT	AGTAGGTGTT	CAATTTTCATT	GGATATTCTT	TTTTTTTAAT	120
TGTCTTTGTA	CCTATGATTG	AAAACAGTAG	TTGGTCTATG	ACTTTTGAGG	AGAGGGAGAA	180
CCGAAGATTA	CAGGAGGCCA	GCATGAGGTT	GGAACAAGAG	AATGATGACC	TTGCCCATGA	240
ACTAGTAACA	AGCAAAATTG	CTCTACGGAA	TGACTTGGAT	CAGGCAGAAG	ACAAGGCAGA	300
TGTGTTGAAT	AAAGAGCTCC	TTTTGACCAA	ACAGAGGCTG	GTGGAGACTG	AAGAGGAGAA	360
GAGGAAGCAA	GAGGAAGAGA	CTGCCCAGCT	AAAAGAAGTC	TTCAGGAAAC	AGCTAGAGAA	420
GGCAGAATAT	GAAATAAAGA	AGACTACAGC	TATCATTTGCT	GAGTATAAAC	AGGTAATGTA	480
CTTCTGTGGC	ACATAGAGCT	AGTTATAGTT	TGCTGCTATA	AAAGTAATTT	TTTTTTTTTT	540
TTGCTTGAGG	CCAGGAGTTT	GAGACTAGCC	TGAGCAACAT	AGCAGGACTC	CGTCCCAAGG	600
AAAAAAAAAA	AAAAAAAAAA					618

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met	Ile	Glu	Asn	Ser	Ser	Trp	Ser	Met	Thr	Phe	Glu	Glu	Arg	Glu	Asn
1			5					10						15	
Arg	Arg	Leu	Gln	Glu	Ala	Ser	Met	Arg	Leu	Glu	Gln	Glu	Asn	Asp	Asp
			20					25					30		
Leu	Ala	His	Glu	Leu	Val	Thr	Ser	Lys	Ile	Ala	Leu	Arg	Asn	Asp	Leu
			35				40					45			
Asp	Gln	Ala	Glu	Asp	Lys	Ala	Asp	Val	Leu	Asn	Lys	Glu	Leu	Leu	Leu
			50			55					60				
Thr	Lys	Gln	Arg	Leu	Val	Glu	Thr	Glu	Glu	Glu	Lys	Arg	Lys	Gln	Glu
65					70				75					80	
Glu	Glu	Thr	Ala	Gln	Leu	Lys	Glu	Val	Phe	Arg	Lys	Gln	Leu	Glu	Lys
				85				90					95		

Ala Glu Tyr Glu Ile Lys Lys Thr Thr Ala Ile Ile Ala Glu Tyr Lys
100 105 110
Gln Val Met Tyr Phe Cys Gly Thr
115 120

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TGCAGAATCC	AGAATGGATG	TCCTCTTTGT	AGCCATCTTT	GCTGTGCCAC	TTATCCTGGG	60
ACAAGAATAT	GAGGATGAAG	AAAGACTGGG	AGAGGATGAA	TATTATCAGG	TGGTCTATTA	120
TTATACAGTC	ACCCCCAGTT	ATGATGACTT	TAGTGCAGAT	TTCACCATTG	ATTACTCCAT	180
ATTTGAGTCA	GAGGACAGGC	TGAACAGGTT	GGATAAGGAC	ATAACAGAAG	CAATAGAGAC	240
TACCATTAGT	CTTGAAACAG	CACGTGCAGA	CCATCCGAAG	CCTGTAAC TG	TGAAACCACT	300
AACAACGGAA	CCTAGTCCAG	ATCTGAACGA	TGCCGTGTCC	AGTTTGCGAA	GTCCTATTCC	360
CCTCCTCCTG	TCGTGTGCCT	TTGTTTCAGG	GGGGATGTAT	TTCATGTAGA	AGGTGGAAGA	420
AGGCTGCTAT	GACTCTTTGG	ATGGGAGTCT	GGCAAGAGGA	AATTGGAAGA	TAAAATAAAT	480
AATAAGTGAA	ATAAAAAAAA	AAAAAAA				510

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Met	Asp	Val	Leu	Phe	Val	Ala	Ile	Phe	Ala	Val	Pro	Leu	Ile	Leu	Gly
1			5					10					15		
Gln	Glu	Tyr	Glu	Asp	Glu	Glu	Arg	Leu	Gly	Glu	Asp	Glu	Tyr	Tyr	Gln
			20					25					30		
Val	Val	Tyr	Tyr	Tyr	Thr	Val	Thr	Pro	Ser	Tyr	Asp	Asp	Phe	Ser	Ala
			35					40					45		
Asp	Phe	Thr	Ile	Asp	Tyr	Ser	Ile	Phe	Glu	Ser	Glu	Asp	Arg	Leu	Asn
			50				55					60			
Arg	Leu	Asp	Lys	Asp	Ile	Thr	Glu	Ala	Ile	Glu	Thr	Thr	Ile	Ser	Leu
			65				70				75				80
Glu	Thr	Ala	Arg	Ala	Asp	His	Pro	Lys	Pro	Val	Thr	Val	Lys	Pro	Val
			85					90						95	
Thr	Thr	Glu	Pro	Ser	Pro	Asp	Leu	Asn	Asp	Ala	Val	Ser	Ser	Leu	Arg
			100					105					110		
Ser	Pro	Ile	Pro	Leu	Leu	Leu	Ser	Cys	Ala	Phe	Val	Gln	Val	Gly	Met
			115				120					125			
Tyr	Phe	Met													
			130												

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 883 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```
CATCTGACCA TCCATATCCA ATGTTCTCAT TTAAACATTA CCCAGCATCA TTGTTTATAA      60
TCAGAACTC TGGTCCTTCT GTCTGGTGGC ACTTAGAGTC TTTTGTGCCA TAATGCAGCA      120
GTATGGAGGG AGGATTTTAT GGAGAAATGG GGATAGTCTT CATGACCACA AATAAATAAA      180
GGAAACTAA GCTGCATTGT GGGTTTGTAA AAGGTTATTA TACTTCTTAA CAATTCTTTT      240
TTTCAGGGAC TTTTCTAGCT GTATGACTGT TACTTGACCT TCTTTGAAAA GCATTCCCAA      300
AATGCTCTAT TTTAGATAGA TTAACATTAA CCAACATAAT TTTTTTTAGA TCGAGTCAGC      360
ATAAATTTCT AAGTCAGCCT CTAGTCGTGG TTCATCTCTT TCACCTGCAT TTTATTTGGT      420
GTTTGTCTGA AGAAAGGAAA GAGGAAAGCA AATACGAATT GTACTATTTG TACCAAATCT      480
TTGGGATTCA TTGGCAAATA ATTTCAAGTGT GGTGTATTAT TAAATAGAAA AAAAAAATTT      540
TGTTTCCTAG GTTGAAGGTC TAATTGATAC GTTTGACTTA TGATGACCAT TTATGCACTT      600
TCAAATGAAT TTGCTTTCAA AATAAATGAA GAGCAGCTGT CCTTCTTTCC TCTTTTAAGT      660
GTTCACTGT GGCATGCTCA GAGGTTCCCTG CTGGATTCCA GCTGGAGCGG TGTGATACCC      720
TTCTTTTTC GCTGTTTCGTG CCTTCCTTTC TTGTATCCAC CAAAGTGGAG ACAAATACAT      780
GATCTCAAAG ATACACAGTA CCTACTTAAT TCCAGCTGAT GGGAGACCAA AGAATTTGCA      840
AGTGGATGGT TTGGTATCAC TGTAAATAAA AAGAGGCCT GGG                               883
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```
Met Met Thr Ile Tyr Ala Leu Ser Asn Glu Phe Ala Phe Lys Ile Asn
1           5           10           15
Glu Glu Gln Leu Ser Phe Phe Pro Leu Leu Ser Val Gln Leu Trp His
20           25           30
Ala Gln Arg Phe Leu Leu Asp Ser Ser Trp Ser Gly Val Ile Pro Phe
35           40           45
Phe Phe Ser Cys Ser Cys Leu Pro Phe Leu Tyr Pro Pro Lys Trp Arg
50           55           60
Gln Ile His Asp Leu Lys Asp Thr Gln Tyr Leu Leu Asn Ser Ser
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      60
AAAAAAAAA AAAAAAAGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA                110
```

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

TAGGCCTCTT TGGCCGGTGC TGCCTGAGAA GGATTGGCAC GGGCACAGAC CACTGCCCCC    60
ACCTGCCCTG CGCCATCTAC CCAAGAAGGC TCGGCACGGG CACCAACCAC TGCCTCCAAC    120
TGCCCCATGC TGCCTGAGAA GGCACGGCAC GGCCACCCCC AACTGCCCCG CACTGTCCCT    180
ACCCGGGCAG CCAATGCGAGC GGCTGGAACCT CTGCTGGCCT TCTGCTGCCT GGTCTTGAGC    240
ACCACTGGGG GCCCTTCCCC AGATACTTGT TCCCAGGACC TTAAGTCACG TGTGAAGCCA    300
GGATTTCCTA AAACAATAAA GACCAATGAC CCAGGAGTCC TCCAAGCAGC CAGATACAGT    360
GTTGAAAAGT TCAACAACCTG CACGAACGAC ATGTTCTTGT TCAAGGAGTC CCGCATCACA    420
AGGGCCCTAG TTCAGATAGT GAAAGGCCCTG AAATATATGC TCGARGTGGA AATTGGCAGA    480
ACTACCTGCA AGAAAAACCA GCACCTGCGT CTGGATGACT GTGACTTCCA AACCAACCAC    540
ACCTTGAAGC AGACTCTGAG CTGCTACTCT GAAGTCTGGG TCGTGCCCTG GCTCCAGCAC    600
TTCGAGGTGC CTGTTCTCCG TTGTCACTGA CCCCCGCCTC TTCAGCAAGA CCACAGCCAT    660
GACAAACACC AGGATGCATG CTCCTTGTCC CCTCCCACCC GCYWSRTGAC CRRRCCTSAC    720
AGACCCTCTC RGGCCTCWGA CGAGTGAGCG GRTGAAGTGC MAYTGGGTSa CMGCAGGGCA    780
GCTRGAATGG CAGCWTGGTA GCGCCTCCTA ACAGRTTAAA TRGATCACAT GTGMTTCTAA    840
AATTRA AAAA AAAAAA A A                                     861
  
```

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Met Leu Pro Glu Lys Ala Leu His Gly His Pro Gln Leu Pro Arg Thr
1           5           10           15
Val Pro Thr Arg Ala Ala Met Arg Ala Ala Gly Thr Leu Leu Ala Phe
20           25           30
Cys Cys Leu Val Leu Ser Thr Thr Gly Gly Pro Ser Pro Asp Thr Cys
35           40           45
Ser Gln Asp Leu Asn Ser Arg Val Lys Pro Gly Phe Pro Lys Thr Ile
50           55           60
Lys Thr Asn Asp Pro Gly Val Leu Gln Ala Ala Arg Tyr Ser Val Glu
65           70           75           80
Lys Phe Asn Asn Cys Thr Asn Asp Met Phe Leu Phe Lys Glu Ser Arg
85           90           95
Ile Thr Arg Ala Leu Val Gln Ile Val Lys Gly Leu Lys Tyr Met Leu
100          105          110
Glu Val Glu Ile Gly Arg Thr Thr Cys Lys Lys Asn Gln His Leu Arg
115          120          125
Leu Asp Asp Cys Asp Phe Gln Thr Asn His Thr Leu Lys Gln Thr Leu
130          135          140
Ser Cys Tyr Ser Glu Val Trp Val Val Pro Trp Leu Gln His Phe Glu
145          150          155          160
Val Pro Val Leu Arg Cys His
165
  
```

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

ANCCAGAATC GGCATCGCTT TTCGAGCTG

29

- (2) INFORMATION FOR SEQ ID NO:199:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TNTGGTGCCT ACTGGATTTC TGGCTTAGA

29

- (2) INFORMATION FOR SEQ ID NO:200:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GNTAACAGAG CTGAATGTTA AACAGGACC

29

- (2) INFORMATION FOR SEQ ID NO:201:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TNTCCTCAAA AGTCATAGAC CAACTACTG

29

- (2) INFORMATION FOR SEQ ID NO:202:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GNTCAGCCTG TCCTCTGACT CAAATATGG

29

- (2) INFORMATION FOR SEQ ID NO:203:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TNACCTGCAT TTTATTTGGT GTTTGTCTG

29

- (2) INFORMATION FOR SEQ ID NO:204:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TNAACACTGT ATCTGGCTGC TTGGAGGAC

29

- (2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GCAAGATTTG GCCTGGATTC TTCTGAGGAT GTGAAGTAAT GGAAACAGTA AGACTGTTCC	60
AGACTAGGGG AAGACTAGAG ACCTAATAGC TGGATTCCAT GTGATCTTTT GTTGGACTTT	120
GGGATTGGAG GTGAGAGTAG AGAAGGCATA ATGCACGTTT TTGAGACGAG GGAAATGTGA	180
ATATAGCCTG TATGCCTACA CTCAAGTCTG AAGACATGTW AACCATGTCT ATACTAACCA	240
GCCAAATATT TGAACACTAA AAGGAAGAAT TTTCTTAATG TGGTAATGGT WTCATGGTTG	300
TATAGAATGT TCCTCCTCTT GGGAGATGTG TGTGAAAAAT AGGGTTTGAC GTCTAAACCT	360
ATTTTGTTTT GGCAAAAAGG ACGTGTGTCT GTACAAAAGA AGTGGAGCCA GTATGGCAAA	420
ATGTTTACMA GGA CTCTGGG TGAGARGTWC ATAGGTGCTT ACTATACTGT TTTGTTTCTG	480
AATTTGGAAT TTCTCAAAAT TAAAAAATA TCTACTGAGG AGCTTTTCGT TTAACTGGT	540
GGGGAATGGG TTCTGGGTGG TTTTGCCCT TTTCTTTTGA GATTCAAGAA ATCCATGGTG	600

AAAGGTTTGG ATTCCATGA AGAAAAGGAG GATAAAGTGA TCAAGGAGAT GGCAGCTCAG	660
ATCCGTGAGG TGGAGCAGAG CCGACAGGAG GTGGTTCGGT CTGTCTTAGA GGTGTTTTC	720
CCTCGGAGGA TCCAGACCAC CTCAGGCAGT GCCAGACCCA GAAGAGGGCT CTTCAGCACC	780
TAGAAGCTGG AAAGGGATGA ACAGGTAAGA CTATTAGGGA ATCTCTTGTT GGGAAATTGA	840
CATCTTAGAA CATTCTGCAA CCTTTTGCCT GGGAAATGGA AACAGATCTA ATCTTTACCA	900
CCCTCATGGC TCAAGGACCT CATCTGGCAG CCTGGCTCAT GTTTTTCAGC CAAGTAGCTT	960
CCAGCTTACA GCAGCCCTCA AATTTGGACC TGCCACCAGC TCCAGAGCTT GACTGGATGG	1020
AGACAGGACC ATCTCTGACA TTCATTGGCC ATCAGGTACA AAGGATAAGC AAGCCAGAAG	1080
AGGGCCAATG GTCCCTCAGG TCTCAGGACC CCTTTCTCCT GATTTTCTAC CTATTCAAGC	1140
CACTGCTGCC TCCACTGCAG GCTTTTCTCTT CTTCCTTCAC TGTTCCTAG TAGTGTTCTC	1200
AGACCTCTTC TCACCCTCCA AAGCGATCCT ATTCACATGT ATTGACACTT AGGAGTGCCA	1260
ACTCCTAAAT CTTGCCCTCT GTAGAACTCA TAGTTCCAAC TCAACACAGG ACATTAAATA	1320
TCCCACAGGC ATCTGAAACT AACCCCCACC ACTCCTATAT TTCCAATCAC TAGATGCAGA	1380
TCCTTTCTCTT TTCCATCTCC CATATCCTGT CAACAAGCGG TCAATTTTAA CCTGTCTGCC	1440
TCCATTACAGC CTTTGGGCAA TTTCTACTCC CCCTTCAATC CTGCCTCACA AACAGAAAAT	1500
CATTGTACCA CTTATGATTT TACTCTACAC TTCAGCTGTA TTGTGTTGCT TCGGGCTTTT	1560
GCAGTTGCCA TTGTCTAAAA CATGCTTTCC TTCCCTCATC ACCTAGTTTA CCTTCAACTG	1620
TTAGCTCAAA TGTCACCTTT TCATAAAAGG CTTATCTGAA CAGGTTATCT CTATTTCAAG	1680
TGGATGTAGC ACCATGTAAA GTTGCAAATG TAATTTACGT AACTTGTGCT TAATGCTCTT	1740
CCCCAATTAT ATGTATGCTG TGAGGGCAAG GTTTTGTCTC CCTGGCATGT AATAGCCACT	1800
CTACTTACAG ACATCTCCAC TGTTATGACT GTGAGCTTCC TGAGGACAGG GTTGTCTTAG	1860
AGTGACTTAC TGTGCTTTCA AAGTTTAACA TCAGCTGGGG TGCAGAATTA GCATTGTGGC	1920
AGCAGTCACA CCCACCTCTT TTAAAGTGTG CTTTGTCTAT CGTTTCTAGG ATTTTTTTTT	1980
TTAATCATGC CTAGACTTTA ACTAGCACTT TTTTCCCAT TTCCAACACT AGGATATAACC	2040
AGGAGTTGGT AACATCCACT CAGGTGCCAC ACCTCCCTGG ATGATCCAAG ATGAAGAATA	2100
CATTGCTGGG AACCAAGAAA TAGGACCATC CTATGAAGAA TTTCTTAAAG AAAAGGAAAA	2160
ACAGAAGTTG AAAAACTCC CCCAGACCG AGTTGGGGCC AACTTTGATC ACAGCTCCAG	2220
GACCAGTGCA GGCTGGCTGC CCTCTTTTGG CCGTGTCTGG AATAATGGAC GCCGCTGGCA	2280

GTCCAGACAT CAATTCAAAA CTGAAGCTGC AGCAATGAAG AAGCAGTCAC ATACAGAAAA 2340
AAGCTAATCA TGCTCTCTAC CAACTACCAT GAGGCTAAAA GCAAAGTCAA CAAACCCCTA 2400
TTATACCTTC CACCAAATTC TTTATCATTG TCTTTCTTAG GAAACAGACA TACTCATTCA 2460
TTTGATTTAA TAAAGTTTTA TTTTTCCTT TGTACAGCTG GTTGGACCTG TAAAAAATAA 2520
TTAAAAGAAT CAGAACCATA AAAAAAAAAA AAAAAA 2556

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met Glu Thr Asp Leu Ile Phe Thr Thr Leu Met Ala Gln Gly Pro His
1 5 10 15
Leu Ala Ala Trp Leu Met Phe Phe Ser Gln Val Ala Ser Ser Leu Gln
20 25 30
Gln Pro Ser Asn Leu Asp Leu Pro Pro Ala Pro Glu Leu Asp Trp Met
35 40 45
Glu Thr Gly Pro Ser Leu Thr Phe Ile Gly His Gln Val Gln Arg Ile
50 55 60
Ser Lys Pro Glu Glu Gly Gln Trp Ser Leu Arg Ser Gln Asp Pro Phe
65 70 75 80
Leu Leu Ile Phe Tyr Leu Phe Lys Pro Leu Leu Pro Pro Leu Gln Ala
85 90 95
Phe Pro Ser Ser Phe Thr Val Pro
100

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TTCATCTTCT CCCTGTA ACT GAGATT TCTA CCACACCTTT GAACAATGTT CTTTCCCTTC	60
TGGTTATCTG AAGACTGTCC TGAAAGGAAG ACATAAGTGT TGTGATTAGT AGAAGCTTTC	120
TAGTAGACCA TATTTCTTCT GGATTGTAAT AAAATTGTTA GTAGCTCCTT TACTTTGTT	180
CCTGTCTCTG GAAAGCCATT TTTGAATTGC TGATTACTTT GGCTTTAATC AGTGGTCACC	240
TAGAAAAAGC TTTGTAATCA TAACACAATG AGTAATTCTT GATAAAAAGT CAGATACAAA	300
AGGAGCACTG TAAACTGGT AGGAGCTATG GTTTAAGAGC ATTGGAAGTA GTTACAAC TC	360
AAGGATTTTG GTAGAAAGGT ATGAGTTTGG TCGAAAAATT AAAATAGTGG CAAAATAAGA	420
TTTAGTTGTG TTTTCTCAGA GCCGCCACAA GATTGAACAA AATGTTTTCT GTTTGGGCAT	480
CCTGAGGAAG TTGTATTAGC TGTTAATGCT CTGTGAGTTT AGAAAAAGTC TTGATAGTAA	540
ATCTAGTTTT TGACACAGTG CATGAACTAA GTAGTTAAAT ATTTACATAT TCAGAAAGGA	600
ATAGTGGAAG AGGTATCTTG GTTATGACAA AGTCATTACA AATGTGACTA AGTCATTACA	660
AATGTGACTG AGTCATTACA GTGGACCCTC TGGGTGCATT GAAAAGAATC CGTTTTATAT	720
CCAGGTTTCA GAGGACCTGG AATAATAATA AGCTTTGGAT TTTGCATTCA GTGTAGTTGG	780
ATTTTGGGAC CTTGGCCTCA GTGTTATTTA CTGGGATTGG CATACGTGTT CACAGGCAGA	840
GTAGTTGATC TCACACAACG GGTGATCTCA CAAACTGGT AAGTTTCTTA TGCTCATGAG	900
CCCTCCCTTT TTTTTTTTAA TTTGGTGCCT GCAACTTTCT TAACAATGAT TCTACTTCCT	960
GGGCTATCAC ATTATAATGC TCTTGGCCTC TTTTTTGCTG CTGTTTTGCT ATTCTTAAAC	1020
TTAGGCCAAG TACCAATGTT GGCTGTTAGA AGGGATTCTG TTCATTCAAC ATGCAACTTT	1080
AGGGAATGGA AGTAAGTTCA TTTTAAAGTT GTGTTGTCAG TAGGTGCGGT GTCTAGGGTA	1140
GTGAATCCTG TAAGTTCAAA TTTATGATTA GGTGACGAGT TGACATTGAG ATTGTCCTTT	1200
TCCCTGATCA AAAAATGAAT AAAGCCTTTT TAAACAAAAA AAAAAAAAAA AAAAAAAAAA	1260
AAAAAAAAAA AAAAAA	1276

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met Ile Leu Leu Pro Gly Leu Ser His Tyr Asn Ala Leu Gly Leu Phe
1 5 10 15
Phe Ala Ala Val Leu Leu Phe Leu Asn Leu Gly Gln Val Pro Met Leu
 20 25 30
Ala Val Arg Arg Asp Ser Val His Ser Thr Cys Asn Phe Arg Glu Trp
 35 40 45
Lys

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGGCTCGTC TGTTCAGGA GCCCTGAACC AAAGAGCAGC GGAGTTTGAG AAGCCAGCAG 60
CTCGGGGTTC GGCAGCAGCG GTCCCATCGG CTGAAGTTTCG GGGGGGGTGG GGCGCCGAGC 120
GCGCGGGGTG GGGGGGGTCC TGGTCTTTGG CTTCTCGACT CGGTCCTGTT TCGACAGCGA 180
ACATGTCGCG GCCTGTCAGA AATAGGAAGG TTGTTGATTA CTCACAGTTT CAGGAATCTG 240
ATGATGCAGA TGAAGATTAT GGAAGAGATT CGGGCCCTCC CACTAAGAAA ATTCGATCAT 300
CTCCCCGAGA AGCTAAAAAT AAGAGGCGAT CTGGAAAGAA TTCACAGGAA GATAGTGAGG 360
ACTCAGAAGA CAAAGATGTG AAGACCAAGA AGGATGATTC TCACTCAGCA GAGGATAGTG 420
AAGATGAAAA AGAAGATCAT AAAAATGTGC GCCAACAACG GCAGGCGGCA TCTAAAGCAG 480
CTTCTAAACA GAGAGAGATG CTCATGGAAG ATGTGGGCAG TGAGGAAGAA CAAGAAGAGG 540
AGGATGAGGC ACCATTCCAG GAGAAAGATT CCGGCAGCGA TGAAGATTTC CTAATGGAAG 600
ATGATGACGA TAGTGA CTAT GGCAGTTCGA AAAAGAAAAA CAAAAGATG GTTAAGAAGT 660
CCAAACCTGA AAGAAAAGAA AAGAAAATGC CCAAACCCAG ACTAAAGGCT ACAGTGACGC 720

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CAAGTCCAGT GAAAGGCAAA GGGAAAGTGG GTCGCCCCAC AGCTTCAAAG GCATCAAAGG      780
AAAAGACTCC TTCTCCCAAA GAAGAAGATG AGGAACCGGA AAGCCCGCCA GAAAAGAAAA      840
CATCTACAAG CCCCCACCC GAGAAATCTG GGGATGAAGG GTCTGAAGAT GAAGCCCCTT      900
CTGGGGAGGA TTAAAAGTGA TGATGGTCTG GGGAGAGATT TTATTAAAAA AAAAAAGAAA      960
AAAAAAGAAA AAAGAGGGAG GAAAAAAAAG AACCTACTTA AGATAGAACA TGGTTTGGC      1020
TATGGCTTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      1080
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA                                     1108

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(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

Met Ser Arg Pro Val Arg Asn Arg Lys Val Val Asp Tyr Ser Gln Phe
1              5              10              15
Gln Glu Ser Asp Asp Ala Asp Glu Asp Tyr Gly Arg Asp Ser Gly Pro
                20              25              30
Pro Thr Lys Lys Ile Arg Ser Ser Pro Arg Glu Ala Lys Asn Lys Arg
                35              40              45
Arg Ser Gly Lys Asn Ser Gln Glu Asp Ser Glu Asp Ser Glu Asp Lys
                50              55              60
Asp Val Lys Thr Lys Lys Asp Asp Ser His Ser Ala Glu Asp Ser Glu
65              70              75              80
Asp Glu Lys Glu Asp His Lys Asn Val Arg Gln Gln Arg Gln Ala Ala
                85              90              95
Ser Lys Ala Ala Ser Lys Gln Arg Glu Met Leu Met Glu Asp Val Gly
                100             105             110
Ser Glu Glu Glu Gln Glu Glu Glu Asp Glu Ala Pro Phe Gln Glu Lys
                115             120             125
Asp Ser Gly Ser Asp Glu Asp Phe Leu Met Glu Asp Asp Asp Asp Ser
                130             135             140
Asp Tyr Gly Ser Ser Lys Lys Lys Asn Lys Lys Met Val Lys Lys Ser

```


145 150 155 160
 Lys Pro Glu Arg Lys Glu Lys Lys Met Pro Lys Pro Arg Leu Lys Ala
 165 170 175
 Thr Val Thr Pro Ser Pro Val Lys Gly Lys Gly Lys Val Gly Arg Pro
 180 185 190
 Thr Ala Ser Lys Ala Ser Lys Glu Lys Thr Pro Ser Pro Lys Glu Glu
 195 200 205
 Asp Glu Glu Pro Glu Ser Pro Pro Glu Lys Lys Thr Ser Thr Ser Pro
 210 215 220
 Pro Pro Glu Lys Ser Gly Asp Glu Gly Ser Glu Asp Glu Ala Pro Ser
 225 230 235 240
 Gly Glu Asp

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2952 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ASTTCRAATT CGGCCTTCAT GGMCTAGCAC GGACTCTGCC TTCTAAAAGT GGAACCCCMC	60
AGTMCCAGCT GTTGCCTMAG SGTGGACASA TCAGSCGAAG CTCCTGCCCT GCCTGTTGGC	120
AGCMTCCATG GGCCAAGCTC TTGCCTCTCA CCATCCTCTC CAGGCCAGT ACTGTTTCCA	180
GCCGGCCTCT CCAGGCCCAA CTCTCCCTCT CAGCTGTGCC TGCCGGCCCA GCTCCTACCT	240
CGCAAAAGCC ACGTTCGGCC CAGCTCCTGC CCAGCTCCTG GCAGCCTTTG TAAACCCAG	300
GATCCTCTAA GTCAGGCCTT TCAGGCCCTG CCTTTGGCTC CCCGGTGGCA TGGAGAGGCC	360
CAGCTCCTGC CTGACAGCGG CCTCTCCAGG CCCAGCTCTT GCCTCACGTT GGCTCCCTG	420
GGCCACGTTT CCGCCTGCCT CGCGGCAGCC CCGACAATCC CGGCTCCTGC CTCCCGATGG	480
CATCTTTAGG CTCATCTCGT GCCTCACCAC GGCCTGCACC AGGCCACACT CCTGCCTTTC	540
GGTGGCCTCC GCGGGCCTGA CTCCTGCGTC CCAATGGCCT CTTTAGGCCC GGCTCGTGCC	600
TCGCCGCGGC CTCCTGAGGC CCACCTTTGC CTTTCTGGCA GCCTCTCCAG GCCCAGGACT	660
TCCTCAAGTC GGCCTCTGCC AGCCCAGTGG CCGCCTCCCG GCCTCCTCTC CGGGCCAGC	720

TCCTTGCTCG TGGCTGCGCC CGCGGGCCCA GTCCTGCCT CTGAACATCC TCCTGTGACT	780
CGGCTCCTGC CCAGCTCCCA GCGGCCCTCCG TAGACCCGAA GCCTCCTCCG GTCCAGCTCT	840
CCAGGCCTGC CTCCTGCCTC GTGGCGGCCT TCCCCGGCCA TGCTCGTGCC GGCTTCCCCG	900
CAGCCTCCAC GAGCCCGGCT CCTGCCTCAC GCGGGCCCCCT CCAGGCCAG CTCGTGCCTC	960
GCGGCGGCCT CTCCAGGCC GGCTCCCGCC CAGCCCGACG GCGTCTCCCA GCCCAAGGCT	1020
CCCTTCCTCA ACGTCGGCCC CTCTGGGCCC AGCTCCTGCC TCCCGCTGAT GGCTGTGCG	1080
GGCCACCCG AGGCGGCCCC AAGTCGGCCT CGCCAGGCC AGCTCCTGCC TGGCGTAGGC	1140
CCCTGGGGG ACGGCCTCTG CCCMACAGTG GCCCTCCGG GCCCAGCTCG TGCCTCGGCT	1200
TGGCCGCTC AGGCCAGCT CCTGCCTGTG GCGGCCTCT CTCCAGACCC GGCTCTCGCC	1260
TCCCGGCATC CTCTCCAGGC CCAGAGCTGT TTCCAGTTGC TAGACCATT TTGTGCCTGC	1320
CTCGTTGCAG CATCTCCAAG CCCAGCTTTT GCTTTTCTGC AGTTTCTTGA GGCCGAATC	1380
CATTTTTCGA ATGGCTTATT TAGGCCAGC TCTTGCCTT GCATTGTCCC TTCAGGCCCA	1440
GAACTTTCTC ACGTCATCGT CACCAGGCCT AGCTTCTGCA TCTGGTCAGC CTTTAAAGGC	1500
CCAGCTTTTG CCTCATAAAC TCAGCTCCTG TTTAATGGCG GCCTCCAGG TCCACCTTC	1560
TGCCTTCCTG TGTCCACTCC AGGCCAGCT ACTGCCTTGG TGCTCTTTT AAGTCAATAA	1620
TTTTTTCCAG TCGACCTCTC CAGGCCCAAC TTGTACCTCT GAGTGTCTC TAGGATCTCA	1680
GCTTCTGCCT AACATGACC TCTTTAGACT CAGCTCATTT TCACTGCTAC ATCTTCAAGC	1740
CATTCCTCTG CCTCTTGGCA ACCTCTAGTG GCCCAGCTTC TGCCTCACAG CAGCCTCTCC	1800
ATGCATGCCT AGCTCCTGCC TCTTTAGGGA ACTTACAGGC CTAAAACTTT CTTAATTTGG	1860
GCTTCTCAAG CCCAGCTCCT GCCTTCTGTT GGGCTCTACA GGCCTGGCAT CATCCTTTCA	1920
ACAGCCTCTT TAGGCCCGGC CTCTCCAGGA CAAAACATC CTTAAGTCAA CCTCACCAGG	1980
CCCGGCTCCT GTCTCCTTGC GGCCTCCAGA GGCCGAGCTT TTGCCTGCCA ATGGCCTCTC	2040
TAGCCCCAGC TTTTGCCTGC CAATGGCCTC TCTAGCCCCA GCTTCTGCCT TTCATCGGTC	2100
TCTCCAGGCT TAGCTCCTTT CTCTTCACGG CCTCTGCAGG CCTAAACTT CCTCAATTTG	2160
GCATCTCCAG GCCCAGCTCC TGCCTCCAGG CCGCCTCTGC AGGCCTATCT CAAGCCTTAC	2220
AACAGCCTCT TTACCCCCAG CTCCTTTCTC CGACTTGTCT CTCCAGGCCT AGAACTTCCT	2280
CATGTTTACC TCACCAGGCC CACCTCCTGC CTTCCAGTAG CGTCTACAAG TTTGGCTCCT	2340
GCCTCCCATG GATCTCTCCA GGCCCCAAAC TTTCTCAAGT CAACCTCACC AGGCCCGGCT	2400
TCTCCCTTTC ATCAGCCTTC CAAAGGCCAG CTTTTGCTTC ATGTCTGCCT TCCGAGTCCC	2460

AGCTCCTGTT TTATGGCAGC CTCCTGAGGC CCAGCTCCTG CCTCCTAGTG GCCTCTTTTG 2520
 GCCCAACTCT TTCCTCACCA GGGCCTTCCA GACCACGTTC CTGCCTTTTA GCAGCCACTA 2580
 CAGGCCCAGC TTTGCGTCCT TTCAAGAGTC CTGCCTCACA GTGGCCTCCC AAGGGCAACT 2640
 TTCTGCCTCA TGTCAGCCTC TTGTGCCCTG GTCCTGCTTC CTGGTAGACT CTGCAGGCCC 2700
 TGCTCCTGCC TTACGTTGCC CCTTTTATAA AGATCCAGTT CCTGCCTCCT GGCTGCCTCT 2760
 ATGAGCCCAA ATCCTGCCTA ACAACAACCT GTTTTTGCC AGCTCCTGCT TCCTGGCAGC 2820
 CTCCTTAGGC CAAAAATTTC CTCAGTTGA CCTCTCCAGG CCCAGCTCCT GCCTCTCAGC 2880
 ACCCTCTTTA GGCCAGCTC CTGCCTTAAT AAATTTGAAT AAATTATTGT TATGTGAAAA 2940
 AAAAAAAAAA AA 2952

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Met Ala Tyr Leu Gly Pro Ala Leu Ala Phe Ala Leu Ser Leu Gln Ala
 1 5 10 15
 Gln Asn Phe Leu Thr Ser Ser Ser Pro Gly Leu Ala Ser Ala Ser Gly
 20 25 30
 Gln Pro Phe Lys Ala Gln Leu Leu Pro His Lys Leu Ser Ser Cys Leu
 35 40 45
 Met Ala Ala Ser Gln Val Pro Pro Ser Ala Phe Leu Cys Pro Leu Gln
 50 55 60
 Ala Gln Leu Leu Pro Trp Cys Ser Phe
 65 70

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GTGCCCCGCC	GCTGCTGTCA	CCCCCGGCCG	CTGCTGCCCT	CCCCGCCGAG	GTTCTACTGC	60
TCTCCTTCTT	AAGAAGGGTG	GGAGGCACTC	GGTCTCTCCC	CACACCTCTC	GCCTGAGGCC	120
AGGCGCCAGG	TGTCGCCTGA	AGCCAGACAG	CCGGTTTGGG	AGCGAGCCTG	AGGTCAACCA	180
ATCAATGGCT	CAGACAGATA	AGCCAACATG	CATCCCGCCG	GAGCTGCCGA	AAATGCTGAA	240
GGAGTTTGCC	AAAGCCGCCA	TTCGGGCGCA	GCCGCAGGAC	CTCATCCAGT	GGGGGGCCGA	300
TTATTTTGAG	GCCCTGTCCC	GTGGAGAGAC	GCCTCCGGTG	AGAGAGCGGT	CTGAGCGAGT	360
CGCTTTGTGT	AACTGGGCAG	AGCTAACACC	TGAGCTGTTA	AAGATCCTGC	ATTCTCAGGT	420
TGCTGGCAGA	CTGATCATCC	GTGCAGAGGA	GCTGGCCCAG	ATGTGGAAG	TGGTGAATCT	480
CCCAACAGAT	CTGTTTAATA	GTGTGATGAA	TGTGGGTCGC	TTCACGGAGG	AGATCGAGTG	540
GCTGAAGTTT	TTAGCCCTTG	CTTGCAGCGC	TCTGGGAGTT	GTAAGTTAGC	TTGACTGTTT	600
TTTGTTCTTG	AAGGGGAAAT	CTCCCTCTGG	GCCTGGAAGG	GCAGTGCATC	TATACACGCG	660
GTCAACTCTG	CAGGGCTGAT	GATAAACATG	CCTCTTCTCC	TATTGTCCTT	CTCCTCTCTA	720
AAGCAAGGTC	ATTTCTGTGC	TCGTCAGGCA	GTGGCAGGGG	TTGGGAGGAG	GAGAGAGGGA	780
AACACTGTGG	TCAGGCTCTG	GGGAGAGTTG	ACTACAGTGT	AGCTCTTGGA	TTATTTATGA	840
ATATTGCCCT	CAGATTTATT	TTCACTCTGC	TCCTTCCATT	CATATTCCCA	GAGACAACCA	900
AGAGCCGACT	GTAGAAAAAG	ACTTCCAGAC	ACCTAGAATA	TATATCAATA	GACACTGTTT	960
AAAAGGGGTA	CAATCTTATA	GAAAACTATG	TAATAAACAG	AATTGGATGC	AGAACTCAGA	1020
CATAAGAAAG	CAAAAACAAA	GAGAGATGAG	GCTATTTCTG	AATTTAGTCA	TGACATCTCC	1080
ATGGATACAG	GATGTTTATA	CAGATTTATG	CCTTTTCCAA	ATTTGACTTG	TTTGATATTG	1140
GAAAAACAAT	TTTACTGTTT	TGAAGCCAAA	GATGTTGAAA	TCAGTTTATA	TGTATAGATA	1200
TTTAAAGCTT	GGGTATCTTA	TATGTGGACT	TACATTGTTA	AACATTGTTA	AAATAAAATG	1260
AATCAAAAAC	ATGGTTTTTTA	AAAAAAAAAA	AAAA			1294

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
Met Ala Gln Thr Asp Lys Pro Thr Cys Ile Pro Pro Glu Leu Pro Lys
1           5           10           15

Met Leu Lys Glu Phe Ala Lys Ala Ala Ile Arg Ala Gln Pro Gln Asp
20           25           30

Leu Ile Gln Trp Gly Ala Asp Tyr Phe Glu Ala Leu Ser Arg Gly Glu
35           40           45

Thr Pro Pro Val Arg Glu Arg Ser Glu Arg Val Ala Leu Cys Asn Trp
50           55           60

Ala Glu Leu Thr Pro Glu Leu Leu Lys Ile Leu His Ser Gln Val Ala
65           70           75           80

Gly Arg Leu Ile Ile Arg Ala Glu Glu Leu Ala Gln Met Trp Lys Val
85           90           95

Val Asn Leu Pro Thr Asp Leu Phe Asn Ser Val Met Asn Val Gly Arg
100          105          110

Phe Thr Glu Glu Ile Glu Trp Leu Lys Phe Leu Ala Leu Ala Cys Ser
115          120          125

Ala Leu Gly Val Val Ser
130
```

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
TTTTTTTTTT TTTTGTATA GCAATGGAAG AATGGCCTCG TACACACGCT AGAGTGGAAA      60
GTCCCAGGCA CCAAGGCTTC CCACCCTAGA AGCAAGCTCA GGGCTTTCTC TTCATCCTTC      120
CAGGGAGAGC ACTGAGAGAT GATGGGGGGT TGGCAGGGGG CATCCCTTGG ATTATCATTC      180
TCCAGACTTA GGCTTGAGAG GGAGGGTGGA GAAGTGGATT TCTGGGTCTG GTCCACCTCA      240
```

CCTGTTTTCT CAGCTTCTCA CCCACTCAGA GCTCTTGCCC CAATTCTCCC TTTCATCCTG 300
 CAGATCCCTG CGCCTGACTC ATCTCAGGCG AGGAGGCAAA TCATCAGTTA TCTCAGGCAG 360
 CAGCAGGACG AGACTCCTTT CTGATTTTCT CCTTCCCTGG CCACCTCTCC CCACCCCAT 420
 TTCACTCATT CCAAACCTCT GGCCTCCCCA GCAACTCTAC ATCCTCATCT CCACCTGTTC 480
 CCTCTCTCGA TGCTGTGGGT GACGTTGGAG AGGGAAGCCC GGAGCCCTGA CCTAGTCCGG 540
 CGTGGAGAGA GGAATGGAAA GCAGTGTCCT TTTTGAGAAG GCAAATTTAC AGCTGGCTTT 600
 TGTAATCCTA GCTATTTTTT GTTTGTTTGC TAAGTCTTTG ATAGTCCCCA GTGTGGTTTG 660
 TCTGCCAGTG ATCTCAGCAC CACCAGAGAG CTTGTTAGAA ATGCGGCATC CCAACCCAC 720
 CACAGCCCTC CCAAGTCAGA TACTGCCACC TCACGAGGCC CCCAGGGAT CCACAAGTTC 780
 ATTAAAGTTT CAGGAATCCA ATTCTACTAC AAAATATACA TTTATAATTA GGAAAAGGAT 840
 AGTTCTTTTA AATGGTAGAA CTTCCCCAAT GAGTCAGCTA CCTGTATTTT TGGCCTGTCA 900
 GGCTAGACAC TGGAGACCAT TCTGCATAGA ATTGTACCTC CCTGAACTAC TGTTAGGCCT 960
 TAGGGTGGGG ATTCATCTTT CCCTTCTCCC CACCATGGAG ACAAATCCT CTTAAACATA 1020
 TCCGGGCTG GCATGGTGGY TMACGCCTCG GCCTCCCAA GTTCTGGGAT TACAGGCATG 1080
 AGCCAYTGTG CCCAGCCACC CGTCACCTGY TAGTGTAGAC AAATGAATAA ACTTAGACAA 1140
 GCACATGGGC TCCCTCTATA CCAGCTAGA CTTTGACACT GAAACTCCAT GAGTCTGGGC 1200
 CACTTCCTGC CACAAGTGTG AATGGAAAAT AAATCATTTT CCAAGGAACC CAAAATCACT 1260
 AAGCCAAGGA GTCAAGCTGA GAACTTTCAG GCAAACCTGC CCCCATT TTTTCTTAA 1320
 TAAGAGAGCT ACAAAGATTA AAAAAAAAAA AAAA 1354

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met Glu Ser Ser Val Pro Phe Glu Lys Ala Asn Leu Gln Leu Ala Phe
 1 5 10 15

Val Ile Leu Ala Ile Phe Cys Leu Phe Ala Lys Ser Leu Ile Val Pro

20	25	30
Ser Val Val Cys Leu Pro Val Ile Ser Ala Pro Pro Glu Ser Leu Leu		
35	40	45
Glu Met Arg His Pro Asn Pro Thr Thr Ala Leu Pro Ser Gln Ile Leu		
50	55	60
Pro Pro His Glu Ala Pro Gln Gly Ser Thr Ser Ser Leu Lys Phe Gln		
65	70	75
Glu Ser Asn Ser Thr Thr Lys Tyr Thr Phe Ile Ile Arg Lys Arg Ile		
85	90	95
Val Leu Leu Asn Gly Arg Thr Ser Pro Met Ser Gln Leu Pro Val Phe		
100	105	110
Leu Ala Cys Gln Ala Arg His Trp Arg Pro Phe Cys Ile Glu Leu Tyr		
115	120	125
Leu Pro Glu Leu Leu Leu Gly Leu Arg Val Gly Ile His Leu Ser Leu		
130	135	140
Leu Pro Thr Met Glu Thr Lys Ser Ser		
145	150	

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CCCCGGTCCC CGCCGCAGCC GCTGCATCCT CCGTGCCCGG CCTGAGCTGG AGTCCCCCGC	60
GCCCCCGCG TTCCGCCCCG CCATGGCTGC GGTGGCGCTG ATGCCACCGC CGCTGCTGCT	120
GCTGCTGCTG TTGGCGTCGC CGCCCGCCGC CTCCGCGCCG TCCGCCCCGCG ATCCCTTCGC	180
CCCCCAGCTC GGGGACACGC AGAACTGCCA GCTGCGGTGC CGCGACCGCG ACCTCGGCCC	240
GCAGCCCTCG CAGGCGGGGC TGGAGGGCGC CTCCGAGTCT CCCTATGACA GAGCCGTTCT	300
GATCAGCGCT TGCGAGCGTG GCTGCCGCCT CTTCTCCATC TGCCGATTG TGGCCAGAAG	360
CTCCAAGCCC AATGCCACCC AAAGTGAGTG TGAAGCAGCC TCGTGGAAG CCTATGTGAA	420
GGAGGCAGAR CAGCAGGCCT GTAGCCACGG CTGCTGGAGC CAGCCCGCGG AGCCTGAGCC	480

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GGARCAGAAG AGAAAGGTCC TGGAGGCTCC AAGTGGGGCC CTCTCCCTCT TGGACTTGTT      540
TTCCACCCTC TGCAATGACC TTGTCAACTC AGCCCAGGGA TTTGTCTCCT CCACCTGGAC      600
ATACTACTTG CAGACTGACA ATGGGAAAGT GGTGGTGT TT CAGACTCAGC CCATAGTGGA      660
GAGCCTCGGC TTCCAGGGGG GCCGTCTGCA GCGCGTGGAG GTGACCTGGC GAGGCTCCCA      720
CCCTGAAGCC CTGGAGGTGC ACGTGGACCC TGTAGGCCCC CTGGACAAGG TGAGGAAGGC      780
CAAGATCCGA GTCAAGACCA GCAGCAAGGC CAAGGTGGAG TCTGAAGAGC CACAGGACAA      840
TGACTTCCTC AGTTGCATGT CCCGGCGCTC GGGTCTGCCT CGCTGGATCC TGGCCTGCTG      900
CCTCTTCCTC TCCGTGCTGG TGATGCTGTG GCTGAGCTGC TCCACCCTGG TGACCGCGCC      960
TGGCCAGCAC CTCAAGTTCC AGCCTCTGAC CCTGGAGCAG CACAAGGGCT TCATGATGGA     1020
GCCCCATTGG CCCCTGTACC CGCCGCCGTC CCACGCCTGT GAGGACAGCC TACCACCCTA     1080
CAAGCTGAAG CTGGACCTGA CCAAGCTGTA GGCCTCCACT GGCCCCATCA CTGCCAACTG     1140
CAGGGGGCCC CTCGGGCCTC ACTTGCCCTG AGCCCAGGAG TCCAAGGGCA GGGTGGGTCC     1200
AGCGTTGAGC CCCTCCACCC CCAAATCCTT CCTCTCCTCC CAGTCCCACC CCTTGCCCCA     1260
CGGAGTCCTG GGGACGCAGT GCCCCAGCTG GGAAGAGGGC GGGATCGGGC ACTGGTTCTT     1320
CCTTGTCCTC GCTTTCCTTG GGGCTTGCTA CTTTTTGTCT TCTATTGTGT GGCTTTCTGA     1380
GTATTTGAAC CCCAGTCCTG TGTCACCTTC CTTTTTCCTT CTATGTCCCC TCTCTGCGGG     1440
GGGGGCGCTG AGGCTGAGGG GGAGCTGCGT CTTGCTAGGG CTTCCCCCTT CTCCCCATCC     1500
CGGTCTCCAG AGACCCAGCT TCTGAGAGAC AGGGTGTGGG CATCTCCATG CCCCTATAAA     1560
GCGTGCCCTG GGCTTGTCCTG GGGCTGGGGA GGAATAAACC ATGTATATAA AAGAAAAAAA     1620
AAAAAAA                                           1628

```

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```

Met Ala Ala Val Ala Leu Met Pro Pro Pro Leu Leu Leu Leu Leu
1              5              10              15

```


Leu Ala Ser Pro Pro Ala Ala Ser Ala Pro Ser Ala Arg Asp Pro Phe
 20 25 30
 Ala Pro Gln Leu Gly Asp Thr Gln Asn Cys Gln Leu Arg Cys Arg Asp
 35 40 45
 Arg Asp Leu Gly Pro Gln Pro Ser Gln Ala Gly Leu Glu Gly Ala Ser
 50 55 60
 Glu Ser Pro Tyr Asp Arg Ala Val Leu Ile Ser Ala Cys Glu Arg Gly
 65 70 75 80
 Cys Arg Leu Phe Ser Ile Cys Arg Phe Val Ala Arg Ser Ser Lys Pro
 85 90 95
 Asn Ala Thr Gln Thr Glu Cys Glu Ala Ala Cys Val Glu Ala Tyr Val
 100 105 110
 Lys Glu Ala Glu Gln Gln Ala Cys Ser His Gly Cys Trp Ser Gln Pro
 115 120 125
 Ala Glu Pro Glu Pro Glu Gln Lys Arg Lys Val Leu Glu Ala Pro Ser
 130 135 140
 Gly Ala Leu Ser Leu Leu Asp Leu Phe Ser Thr Leu Cys Asn Asp Leu
 145 150 155 160
 Val Asn Ser Ala Gln Gly Phe Val Ser Ser Thr Trp Thr Tyr Tyr Leu
 165 170 175
 Gln Thr Asp Asn Gly Lys Val Val Val Phe Gln Thr Gln Pro Ile Val
 180 185 190
 Glu Ser Leu Gly Phe Gln Gly Gly Arg Leu Gln Arg Val Glu Val Thr
 195 200 205
 Trp Arg Gly Ser His Pro Glu Ala Leu Glu Val His Val Asp Pro Val
 210 215 220
 Gly Pro Leu Asp Lys Val Arg Lys Ala Lys Ile Arg Val Lys Thr Ser
 225 230 235 240
 Ser Lys Ala Lys Val Glu Ser Glu Glu Pro Gln Asp Asn Asp Phe Leu
 245 250 255
 Ser Cys Met Ser Arg Arg Ser Gly Leu Pro Arg Trp Ile Leu Ala Cys
 260 265 270
 Cys Leu Phe Leu Ser Val Leu Val Met Leu Trp Leu Ser Cys Ser Thr
 275 280 285
 Leu Val Thr Ala Pro Gly Gln His Leu Lys Phe Gln Pro Leu Thr Leu
 290 295 300
 Glu Gln His Lys Gly Phe Met Met Glu Pro Asp Trp Pro Leu Tyr Pro
 305 310 315 320

Pro Pro Ser His Ala Cys Glu Asp Ser Leu Pro Pro Tyr Lys Leu Lys
325 330 335

Leu Asp Leu Thr Lys Leu
340

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 671 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCGGGCGGCG GAGTAGCAAG TGGCCATGGG GAGCCTCAGC GGTCTGCGCC TGGCAGCAGG	60
AAGCTGTTTT AGGTTATGTG AAAGAGATGT TTCCTCATCT CTAAGGCTTA CCAGAAGCTC	120
TGATTTGAAG AGAATAAATG GATTTTGCAC AAAACCACAG GAAAGTCCCG GAGCTCCATC	180
CCGCACTTAC AACAGAGTGC CTTTACACAA ACCTACGGAT TGGCAGAAAA AGATCCTCAT	240
ATGGTCAGGT CGCTTCAAAA AGGAAGATGA AATCCCAGAG ACTGTCTCGT TGGAGATGCT	300
TGATGCTGCA AAGAACAAGA TGCGAGTGAA GATCAGCTAT CTAATGATTG CCCTGACGGT	360
GGTAGGATGC ATCTTCATGG TTATTGAGGG CAAGAAGGCT GCCCAAAGAC ACGAGACTTT	420
AACAAGCTTG AACTTAGAAA AGAAAGCTCG TCTGAAAGAG GAAGCAGCTA TGAAGGCCAA	480
AACAGAGTAG CAGAGGTATC CGTGTTGGCT GGATTTTGAA AATCCAGGAA TTATGTTATA	540
ACGTGCCTGT ATTAAAAAGG ATGTGGTATG AGGATCCATT TCATAAAGTA TGATTTGCCC	600
AAACCTGTAC CATTTCCGTA TTTCTGCTGT AGAAGTAGAA ATAAATTTTC TTAAATAAAA	660
AAAAAAAAAA A	671

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg
1 5 10 15
Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser
20 25 30
Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
35 40 45
Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
50 55 60
Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu
65 70 75 80
Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys
85 90 95
Asn Lys Met Arg Val Lys Ile Ser Tyr Leu Met Ile Ala Leu Thr Val
100 105 110
Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg
115 120 125
His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys
130 135 140
Glu Glu Ala Ala Met Lys Ala Lys Thr Glu
145 150

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1056 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CACAAGAGGA GTTACTTGTT CCAGCCTCCT GTGTGGACTG CTTTCCTATC AAAGCACCTT 60
AGACATGCAC GAGGAAGAAA TATACACCTC TCTTCAGTGG GATAGCCCAG CACCAGACAC 120
TTACCAGAAA TGTCTGTCTT CCAACAAATG TTCAGGAGCA TGCTGTCTTG TGATGGTGAT 180
TTCATGTGTT TTCTGCATGG GATTATTAAC GGCATCCATT TTCTTGGGCG TCAAGTTGTT 240
GCAGGTGTCC ACCATTGCGA TGCAGCAGCA AGAAAACTC ATCCAACAAG AGAGGGCACT 300

GCTAAACTTT ACAGAATGGA AGAGAAGCTG TGCCCTTCAG ATGAAATATT GCCAAGCCTT 360
CATGCAAAAC TCATTAAGTT CAGGATTTTA TCACTGGCAG CTTGAGGAAG ATTAAAGGAA 420
GCTATGATTA CTGGGTGGGG TTGTCTCAGG ATGGACACAG CGGACGCTGG CTTTGGCAAG 480
ATGGCTCCTC TCCTTCTCCT GGCCTGTTGC CAGCAGAGAG ATCCCAGTCA GCTAACCAAG 540
TCTGTGGATA CGTGAAAAGC AATTCCCTTC TTTCGTCTAA CTGCAGCACG TGGAAGTATT 600
TTATCTGTGA GAAGTATGCG TTGAGATCCT CTGTCTGAAA GAAATTGTGT TCAAAGTGTT 660
CTATTACACT GTTATTTTGA GCATGCCATT GGAAAACCCA CCCCCACCCC CCCTCAAAAA 720
AACAGAACAG TAAACCAAAA TGTGGGCCAT GAAATTAGCA ACCTGGGACT CAATAATACA 780
CTTGGGAATA TTCTTCCACA CCGTCCAGAT TTCATTTGAT GTTGTTTACA TTGCAAGAGT 840
AAAAC TTATT TAGAGCTACA GAAGACAAAA CCCTGAAGAG TTAAGAACAA ACGCAAGGAA 900
ATAATTTTTTA TTGTTTAAAG CCCGGAATGA CTGTAACTTT CACACAAGGT ACGCATCTAT 960
GTTTTTTGGGG GAGGTGATGT AGTTACAGCT GACTAATATT TTTAAAATAA ATAAATAAAT 1020
TTGGCCTTTA AAACTCAAAA AAAAAAAAAA AAAAAA 1056

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met	His	Glu	Glu	Glu	Ile	Tyr	Thr	Ser	Leu	Gln	Trp	Asp	Ser	Pro	Ala
1				5					10					15	
Pro	Asp	Thr	Tyr	Gln	Lys	Cys	Leu	Ser	Ser	Asn	Lys	Cys	Ser	Gly	Ala
			20					25					30		
Cys	Cys	Leu	Val	Met	Val	Ile	Ser	Cys	Val	Phe	Cys	Met	Gly	Leu	Leu
		35					40					45			
Thr	Ala	Ser	Ile	Phe	Leu	Gly	Val	Lys	Leu	Leu	Gln	Val	Ser	Thr	Ile
	50					55					60				
Ala	Met	Gln	Gln	Gln	Glu	Lys	Leu	Ile	Gln	Gln	Glu	Arg	Ala	Leu	Leu
65					70				75					80	
Asn	Phe	Thr	Glu	Trp	Lys	Arg	Ser	Cys	Ala	Leu	Gln	Met	Lys	Tyr	Cys
				85					90					95	

Gln Ala Phe Met Gln Asn Ser Leu Ser Ser Gly Phe Tyr His Trp Gln
 100 105 110

Leu Glu Glu Asp
 115

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

ANATTAGATC TGTTTCCATT TCCCAGGCA

29

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNGCGTGAGA TCAACTACTC TGCCTGTGA

29

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

ANACAGGACC GAGTCGAGAA GCCAAAGAC

29

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

ANGGGACAAT GCAAACGCAA GAGCTGGGC

29

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ANGAGGCATG TTTATCATCA GCCCTGCAG

29

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

ANATTTGCCT TCTCAAAAGG GACACTGCT

29

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GNTGGGACTG GGAGGAGAGG AAGGATTTG

29

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GNAACGCCAT AAGCATGTCC TTCTAATGT

29

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CNTGAAATCA CCATCACAAG ACAGCATGC

29